

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Boon-Falleur, Thierry; Van der Bruggen, Thierry; Van den Eynde, Benoît; Van Pel, Aline; De Plaen, Etienne; Lurquin, Christophe; Chomez, Patrick; Traversari, Catia
- (ii) TITLE OF INVENTION: Tumor Rejection Antigen Precursors, Tumor Rejection Antigens and Uses Thereof
- (iii) NUMBER OF \SEQUENCES: 26
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Fulbright & Jaworski LLP
 - (B) STREET: 666 Fifth Avenue
 - (C) CITY: New York City
 - (D) STATE: New York
 - (E) COUNTRY; USA
 - (F) ZIP: 10103
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
 - (B) COMPUTER: \IBM
 - (C) OPERATING SYSTEM: PC-DOS
 - (D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/819,669
 - (B) FILING DATE: \17-March-1997
 - (C) CLASSIFICATION: 435
- (vii) PRIOR APPLIATION DATA:
 - (A) APPLICATION NUMBER: 08/142,368
 - (B) FILING DATE: 0\2-MAY-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US92/04354
 - (B) FILING DATE: 22-MAY-1992
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/807,043
 - (B) FILING DATE: 12-DECEMBER-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 07/764,364
 - (B) FILING DATE: 23-SEPTEMBER-1991
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: \07/728,838
 - (b) FILING DATE: 9-JULY 1991
- (vii) PRIOR APPLICATION DATA:

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(B) FILING DATE 23-May-1991 (viii) ATTORNEY/AGENT\ INFORMATION: (A) NAME: Hanson, Norman D. (B) REGISTRATION \NUMBER: 30,946 (C) REFERENCE/DOCKET NUMBER: LUD 5253.5-US (ix) TELECOMMUNICATION \INFORMATION: (A) TELEPHONE: (21/2)318-3168 (B) TELEFAX: (212) 752-5958 INFORMATION FOR SEQUENCE \ID NO: 1: (2) (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 462 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1: ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTGT GAAGATCCTG 60 ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCCT CAGCCAATGA GCTTACTGTT 120 CTCGTGGGGG GTTTGTGAGC CTTGGGTAGG AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG 180 CTTGTGAATT TGTACCCTTT CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC 240 CCCCCTCCCA CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTAT 300 AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCAG CATGCATTGT 360 420 TATCTTAACT TAGCTCGGCT TCCTGCTGGT ACCCTTTGTG CC 462 (2) INFORMATION FOR SEQUENCE ID NO: 2: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 675 base pairs (B) TYPE: nucleic acid(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2: ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT 'GGC TCA GGT GGT Met Ser Asp Asn Lys Lys Pro Asp Lys Ala His Ser Gly Ser Gly Gly 5 15 10 96 GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC CGG TAC TCC CTG GAA

(A) APPLICATION NUMBER: 07/705,702

576670.1

Asp	Gly	Asp	Gly 20	Asn	Arg	Cys	Asn	Leu 25	Leu	His	Arg	Tyr	Ser 30	Leu	Glu	
				TAT Tyr												144
		CTG		CTC Leu			TTC					TAT				192
				GTG Val												240
				GAT Asp 85												288
				GAC Asp												336
				TTG Leu												384
				ATG Met												432
				AAC Asn												480
AAT				TGT Cys 165											TTC	528
				CCA Pro												576
				GAA Glu												624
				GAA Glu												672
TAG																675

(2) INFORMATION FOR SEQUENCE ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 base pairs (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: genomic DNA
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

GCATGCAGTT	GCAAAGCCCA	GAAGAAAGAA	ATGGACAGCG	GAAGAAGTGG	TTGTTTTTTT	60
TTCCCCTTCA	TTAATTTTCT	AGTTTTTAGT	AATCCAGAAA	ATTTGATTTT	GTTCTAAAGT	120
TCATTATGCA	AAGATGTCAC	CAACAGACTT	CTGACTGCAT	GGTGAACTTT	CATATGATAC	180
ATAGGATTAC	ACTTGTACCT	GTTAAAAATA	AAAGTTTGAC	TTGCATAC		228

- (2) INFORMATION FOR SEQUENCE ID NO: 4:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1365 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CTAGATGTC	3T 50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT ATTCATCCC	CT 100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CTTGGGTAC	GG 150
AAGTTTTGCA AGTTCCGCCT ACAGCTCTAG CTTGTGAATT TGTACCCTT	TT 200
CACGTAAAAA AGTAGTCCAG AGTTTACTAC ACCCTCCCTC CCCCCTCCC	CA 250
CCTCGTGCTG TGCTGAGTTT AGAAGTCTTC CTTATAGAAG TCTTCCGTA	AT 300
AGAACTCTTC CGGAGGAAGG AGGGAGGACC CCCCCCTTT GCTCTCCCA	AG 350
CATGCATTGT GTCAACGCCA TTGCACTGAG CTGGTCGAAG AAGTAAGCC	CG 400
CTAGCTTGCG ACTCTACTCT TATCTTAACT TAGCTCGGCT TCCTGCTGC	GT 450
ACCCTTTGTG CC	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AGT GGC	ΓCA 504
GGT GGT GAC GGT GAT GGG AAT AGG TGC AAT TTA TTG CAC (CGG 546
100 010 0 0 010 001 1 0111 0111 0111	GTC 588
	TTC 630
	GCC 672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GTC GAT C	GAG 714
	GAC 756
GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GAG GAT C	GAT 798
GAG GAA GAA TTG GAG AAC CTG ATG GAT GAA TCA C	
	GGA 882
	CCT 924
	ATT 966
TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT ATA CCA C	
AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA AAT GCT C	
GAA GAG GTT GCA ATG GAA GAA GAA GAA GAA GAG GAG G	
GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC TTC TCA C	
TAG	1137
GCATGCAGTT GCAAAGCCCA GAAGAAAGAA ATGGACAGCG GAAGAAGTC	
TTGTTTTTT TTCCCCTTCA TTAATTTTCT AGTTTTTAGT AATCCAGA	
ATTTGATTTT GTTCTAAAGT TCATTATGCA AAGATGTCAC CAACAGACT	
CTGACTGCAT GGTGAACTTT CATATGATAC ATAGGATTAC ACTTGTACC	
GTTAAAAATA AAAGTTTGAC TTGCATAC	1365

- (2) INFORMATION FOR SEQUENCE ID NO: 5:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4698 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ACCACAGGAG AATGAAAAGA ACCCGGGACT CCCAAAGACG CT	AGATGTGT	50
GAAGATCCTG ATCACTCATT GGGTGTCTGA GTTCTGCGAT AT	TCATCCCT	100
CAGCCAATGA GCTTACTGTT CTCGTGGGGG GTTTGTGAGC CT	TGGGTAGG	150
	TACCCTTT	200
	CCCTCCCA	250
	TTCCGTAT	300
	TCTCCCAG	350
	GTAAGCCG	400
	CTGCTGGT	450
ACCCTTTGTG CC	CIUCIUUI	462
ATG TCT GAT AAC AAG AAA CCA GAC AAA GCC CAC AG	T GGC TCA	504
	G CAC CGG	546
	G CTG GTC	588
		630
ATA GAC GCC CTT TAT GAG GAG CAG TAT GAA AGG GA		672
TGG ATA GCC AGG CAA AGC AAG CGC ATG TCC TCT GT		714
GAT GAA GAC GAT GAG GAT GAT GAC TAC TA		756
GAG GAC GAC GAC GAT GCC TTC TAT GAT GAT GA		798
	A TCA GAA	840
*	T GCC GGA	882
GCT GAG GAA ATG GGT GCT GGC GCT AAC TGT GCC T		916
	ATTCTTTA	966
	GTCATTGC	1016
	CTCCCATC	1066
	TCTGGAGC	1116
TTCAGTCCAT CCTGCTCTGC TCCCTTTCCC CTTTGCTCTC CT	TGCTCCCC	1166
	CCACCCTC	1216
	CCTGTTCC	1266
CCTTTTCGCG CCTTTTCTTT CCTGCTCCCC TCCCCCTCCC TA	TTTACCTT	1316
TCACCAGCTT TGCTCTCCCT GCTCCCCTCC CCCTTTTGCA CC	TTTTCTTT	1366
TCCTGCTCCC CTCCCCTCC CCTCCCTGTT TACCCTTCAC CG	CTTTTCCT	1416
CTACCTGCTT CCCTCCCCT TGCTGCTCCC TCCCTATTTG CA	TTTTCGGG	1466
TGCTCCTCCC TCCCCCTCCC CCTCCCTCCC TATTTGCATT TT	CGGGTGCT	1516
CCTCCCTCCC CCTCCCCAGG CCTTTTTTTT TTTTTTTTT TT	$\operatorname{TTTTTTT}$	1566
TTGGTTTTTC GAGACAGGGT TTCTCTTTGT ATCCCTGGCT GT	CCTGGCAC	1616
TCACTCTGTA GACCAGGCTG GCCTCAAACT CAGAAATCTG CC	TGCCTCTG	1666
CCTCCCAAAT GCTGGGATTA AAGGCTTGCA CCAGGACTGC CC	CAGTGCAG	1716
GCCTTTCTTT TTTCTCCTCT CTGGTCTCCC TAATCCCTTT TC	TGCATGTT	1766
AACTCCCCTT TTGGCACCTT TCCTTTACAG GACCCCCTCC CC	CTCCCTGT	1816
TTCCCTTCCG GCACCCTTCC TAGCCCTGCT CTGTTCCCTC TC	CCTGCTCC	1866
CCTCCCCCTC TTTGCTCGAC TTTTAGCAGC CTTACCTCTC CC	TGCTTTCT	1916
	CACCTTCC	1966
	GCTTTTTT	2016
	CGGCTTCC	2066
	CCTCCCTT	2116
	ATGCCTTT	2166
	GCACTTTT	2216
	CCCACCTC	2266
	CTCCCACT	2316
	GCCTGCTG	2366
Totalica Timeccell ecolorect merered of		200

	0416
GACTTCCTCT CCAGCCGCCC AGTTCCCTGC AGTCCTGGAG TCTTTCCTGC	2416
CTCTCTGTCC ATCACTTCCC CCTAGTTTCA CTTCCCTTTC ACTCTCCCCT	2466
ATGTGTCTCT CTTCCTATCT ATCCCTTCCT TTCTGTCCCC TCTCCTCTGT	2516
CCATCACCTC TCTCCTCCCT TCCCTTTCCT CTCTCTTCCA TTTTCTTCCA	2566
CCTGCTTCTT TACCCTGCCT CTCCCATTGC CCTCTTACCT TTATGCCCAT	2616
TCCATGTCCC CTCTCAATTC CCTGTCCCAT TGTGCTCCCT CACATCTTCC	2666
ATTTCCCTCT TTCTCCCTTA GCCTCTTCTT CCTCTTCTCT TGTATCTCCC	2716
TTCCCTTTGC TTCTCCCTCC TCCTTTCCCC TTCCCCTATG CCCTCTACTC	2766
TACTTGATCT TCTCTCCTCT CCACATACCC TTTTTCCTTT CCACCCTGCC	2816
CTTTGTCCCC AGACCCTACA GTATCCTGTG CACAGGAAGT GGGAGGTGCC	2866
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AAGGCTGGAT GAAAATAAGG CCAGGTTCTG AGGACAGCTG GAATCTAGCC	2966
AAGTGGCTCC TATAACCCTA AGTACCAAGG GAGAAAGTGA TGGTGAAGTT	3016
CTTGATCCTT GCTGCTTCTT TTACATATGT TGGCACATCT TTCTCAAATG	3066
CAGGCCATGC TCCATGCTTG GCGCTTGCTC AGCGTGGTTA AGTAATGGGA	
	3116
GAATCTGAAA ACTAGGGGCC AGTGGTTTGT TTTGGGGACA AATTAGCACG	3166
TAGTGATATT TCCCCCTAAA AATTATAACA AACAGATTCA TGATTTGAGA	3216
TCCTTCTACA GGTGAGAAGT GGAAAAATTG TCACTATGAA GTTCTTTTTA	3266
GGCTAAAGAT ACTTGGAACC ATAGAAGCGT TGTTAAAATA CTGCTTTCTT	3316
TTGCTAAAAT ATTCTTTCTC ACATATTCAT ATTCTCCAG	3355
GT GTT CCT GGC CAT CAT TTA AGG AAG AAT GAA GTG AAG TGT	3396
AGG ATG ATT TAT TTC TTC CAC GAC CCT AAT TTC CTG GTG TCT	3438
ATA CCA GTG AAC CCT AAG GAA CAA ATG GAG TGT AGG TGT GAA	3480
AAT GCT GAT GAA GAG GTT GCA ATG GAA GAG GAA GAA GAA	3522
GAG GAG GAG GAG GAA GAG GAA ATG GGA AAC CCG GAT GGC	3564
TTC TCA CCT TAG	3576
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA	3626
GCATGCAGGT ACTGGCTTCA CTAACCAACC ATTCCTAACA TATGCCTGTA	3626 3676
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA	3676
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA	3676 3726
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT	3676 3726 3776
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA	3676 3726 3776 3826
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG	3676 3726 3776 3826 3876
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT	3676 3726 3776 3826 3876 3926
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG	3676 3726 3776 3826 3876 3926 3976
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT	3676 3726 3776 3826 3876 3926 3976 4026
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT	3676 3726 3776 3826 3876 3926 3976
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT	3676 3726 3776 3826 3876 3926 3976 4026
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT	3676 3726 3776 3826 3876 3926 3976 4026 4076
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAG GATTTCTTAA	3676 3726 3776 3826 3876 3926 3976 4026 4076 4126
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTCCAT TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA	3676 3726 3776 3826 3876 3926 3976 4026 4076 4126 4176
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA	3676 3726 3776 3826 3876 3926 3976 4026 4076 4126 4176 4226
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTTCATC TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC	3676 3726 3776 3826 3876 3926 4026 4076 4126 4176 4226 4276 4326
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTTCAATC TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT	3676 3726 3776 3826 3876 3926 3976 4026 4076 4126 4176 4226 4276 4326 4376
GCTAAGAGCA TCTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA	3676 3726 3776 3826 3876 3926 3976 4026 4076 4126 4176 4226 4276 4376 4426
GCTAAGAGCA TCTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTTCATC TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA AGTCAGGGGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC	3676 3726 3776 3826 3876 3926 3976 4026 4076 4126 4276 4276 4326 4376 4426 4476
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTCAATC TAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT	3676 3726 3776 3826 3876 3926 3976 4026 4176 4126 4176 4226 4376 4326 4476 4526
GCTAAGAGCA TCTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTT TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA	3676 3726 3776 3826 3876 3926 3976 4026 4176 4226 4276 4326 4376 4476 4526 4576
GCTAAGAGCA TCTTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAAATTCT TAATTCAATC TAACTTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAAACCA ACAGGGAAAT ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTTT TTTTTTCCCC TTCATTAATT TCTTAGTTTT TAGTAATCCA GAAAATTTGA TTTTTTTCCCC TTCATTAATT TCCTAGTTTT TAGTAATCCA GAAAATTTGA TTTTTTTCTCTA AAGTTTCATTA TGCAAAGATG TCACCAACAG ACTTCTGACT	3676 3726 3776 3826 3876 3926 3976 4026 4076 4126 4276 4226 4276 4376 4426 4476 4526 4576 4626
GCTAAGAGCA TCTTTTAAA AAATATTATT GGTAAACTAA ACAATTGTTA TCTTTTTACA TTAATAAGTA TTAAATTAAT CCAGTATACA GTTTTAAGAA CCCTAAGTTA AACAGAAGTC AATGATGTCT AGATGCCTGT TCTTTAGATT GTAGTGAGAC TACTTACTAC AGATGAGAAG TTGTTAGACT CGGGAGTAGA GACCAGTAAA AGATCATGCA GTGAAATGTG GCCATGGAAA TCGCATATTG TTCTTATAGT ACCTTTGAGA CAGCTGATAA CAGCTGACAA AAATAAGTGT TTCAAGAAAG ATCACACGCC ATGGTCACA TGCAAATTAT TATTTTGTCG TTCTGATTTT TTTCATTCT AGACCTGTGG TTTTAAAGAG ATGAAAATCT CTTAAAATTT CCTTCATCTT TAATTTCCT TAACTTTAGT TTTTTTCACT TAGAATTCAA TTCAAATTCT TAATTCAATC TTAATTTTTA GATTTCTTAA AATGTTTTTT AAAAAAAATG CAAATCTCAT TTTTAAGAGA TGAAAGCAGA GTAACTGGGG GGCTTAGGGA ATCTGTAGG TTGCGGTATA GCAATAGGGA GTTCTGGTCT CTGAGAAGCA GTCAGAGAGA ATGGAAAACC AGGCCCTTGC CAGTAGGTTA GTGAGGTTGA TATGATCAGA TTATGGACAC TCTCCAAATC ATAAATACTC TAACAGCTAA GGATCTCTGA GGGAAACACA ACAGGGAAAT ATTTTAGTTT CTCCTTGAGA AACAATGACA AGACATAAAA TTGGCAAGAA AGTCAGGAGT GTATTCTAAT AAGTGTTGCT TATCTCTTAT TTTCTTCTAC AGTTGCAAAG CCCAGAAGAA AGAAATGGAC AGCGGAAGAA GTGGTTGTT TTTTTTCCCC TTCATTAATT TTCTAGTTTT TAGTAATCCA GAAAATTTGA	3676 3726 3776 3826 3876 3926 3976 4026 4176 4226 4276 4326 4376 4476 4526 4576

- (2) INFORMATION FOR SEQUENCE ID NO: 6:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Leu Pro Tyr Leu Gly Trp Leu Val Phe 5

- (2) INFORMATION FOR SEQUENCE ID NO: 7:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2419 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGATCCAGGC	CCTGCCAGGA	AAAATATAAG	GGCCCTGCGT	GAGAACAGAG	50
GGGGTCATCC	ACTGCATGAG	AGTGGGGATG	TCACAGAGTC	CAGCCCACCC	100
TCCTGGTAGC	ACTGAGAAGC	CAGGGCTGTG	CTTGCGGTCT	GCACCCTGAG	150
GGCCCGTGGA	TTCCTCTTCC	TGGAGCTCCA	GGAACCAGGC	AGTGAGGCCT	200
TGGTCTGAGA	CAGTATCCTC	AGGTCACAGA	GCAGAGGATG	CACAGGGTGT	250
GCCAGCAGTG	AATGTTTGCC	CTGAATGCAC	ACCAAGGGCC	CCACCTGCCA	300
CAGGACACAT	AGGACTCCAC	AGAGTCTGGC	CTCACCTCCC	TACTGTCAGT	350
CCTGTAGAAT	CGACCTCTGC	TGGCCGGCTG	TACCCTGAGT	ACCCTCTCAC	400
TTCCTCCTTC	AGGTTTTCAG	GGGACAGGCC	AACCCAGAGG	ACAGGATTCC	450
CTGGAGGCCA	CAGAGGAGCA	CCAAGGAGAA	GATCTGTAAG	TAGGCCTTTG	500
TTAGAGTCTC	CAAGGTTCAG	TTCTCAGCTG	AGGCCTCTCA	CACACTCCCT	550
CTCTCCCCAG	GCCTGTGGGT	CTTCATTGCC	CAGCTCCTGC	CCACACTCCT	600
GCCTGCTGCC	CTGACGAGAG	TCATCATGTC	TCTTGAGCAG	AGGAGTCTGC	650
ACTGCAAGCC	TGAGGAAGCC	CTTGAGGCCC	AACAAGAGGC	CCTGGGCCTG	700
GTGTGTGTGC	AGGCTGCCAC	CTCCTCCTCC	TCTCCTCTGG	TCCTGGGCAC	750
CCTGGAGGAG	GTGCCCACTG	CTGGGTCAAC	AGATCCTCCC	CAGAGTCCTC	800
AGGGAGCCTC	CGCCTTTCCC	ACTACCATCA	ACTTCACTCG	ACAGAGGCAA	850
CCCAGTGAGG	GTTCCAGCAG	CCGTGAAGAG	GAGGGGCCAA	GCACCTCTTG	900
TATCCTGGAG	TCCTTGTTCC	GAGCAGTAAT	CACTAAGAAG	GTGGCTGATT	950
TGGTTGGTTT	TCTGCTCCTC	AAATATCGAG	CCAGGGAGCC	AGTCACAAAG	1000
GCAGAAATGC	TGGAGAGTGT	CATCAAAAAT	TACAAGCACT	GTTTTCCTGA	1050
GATCTTCGGC	AAAGCCTCTG	AGTCCTTGCA	GCTGGTCTTT	GGCATTGACG	1100
TGAAGGAAGC	AGACCCCACC	GGCCACTCCT	ATGTCCTTGT	CACCTGCCTA	1150
GGTCTCTCCT	ATGATGGCCT	GCTGGGTGAT	AATCAGATCA	TGCCCAAGAC	1200
AGGCTTCCTG	ATAATTGTCC	TGGTCATGAT	TGCAATGGAG	GGCGGCCATG	1250
CTCCTGAGGA	GGAAATCTGG	GAGGAGCTGA	GTGTGATGGA	GGTGTATGAT	1300
GGGAGGAGC	ACAGTGCCTA	TGGGGAGCCC	AGGAAGCTGC	TCACCCAAGA	1350
TTTGGTGCAG	GAAAAGTACC	TGGAGTACGG	CAGGTGCCGG	ACAGTGATCC	1400

CGCACGCTAT	GAGTTCCTGT	GGGGTCCAAG	GGCCCTCGCT	GAAACCAGCT	1450
ATGTGAAAGT	CCTTGAGTAT	GTGATCAAGG	TCAGTGCAAG	AGTTCGCTTT	1500
TTCTTCCCAT	CCCTGCGTGA	AGCAGCTTTG	AGAGAGGAGG	AAGAGGGAGT	1550
CTGAGCATGA	GTTGCAGCCA	AGGCCAGTGG	GAGGGGGACT	GGGCCAGTGC	1600
ACCTTCCAGG	GCCGCGTCCA	GCAGCTTCCC	CTGCCTCGTG	TGACATGAGG	1650
CCCATTCTTC	ACTCTGAAGA	GAGCGGTCAG	TGTTCTCAGT	AGTAGGTTTC	1700
TGTTCTATTG	GGTGACTTGG	AGATTTATCT	TTGTTCTCTT	TTGGAATTGT	1750
TCAAATGTTT	TTTTTTAAGG	GATGGTTGAA	TGAACTTCAG	CATCCAAGTT	1800
TATGAATGAC	AGCAGTCACA	CAGTTCTGTG	TATATAGTTT	AAGGGTAAGA	1850
GTCTTGTGTT	TTATTCAGAT	TGGGAAATCC	ATTCTATTTT	GTGAATTGGG	1900
ATAATAACAG	CAGTGGAATA	AGTACTTAGA	AATGTGAAAA	ATGAGCAGTA	1950
AAATAGATGA	GATAAAGAAC	TAAAGAAATT	AAGAGATAGT	CAATTCTTGC	2000
CTTATACCTC	AGTCTATTCT	GTAAAATTTT	TAAAGATATA	TGCATACCTG	2050
GATTTCCTTG	GCTTCTTTGA	GAATGTAAGA	GAAATTAAAT	CTGAATAAAG	2100
AATTCTTCCT	GTTCACTGGC	TCTTTTCTTC	TCCATGCACT	GAGCATCTGC	2150
TTTTTGGAAG	GCCCTGGGTT	AGTAGTGGAG	ATGCTAAGGT	AAGCCAGACT	2200
CATACCCACC	CATAGGGTCG	TAGAGTCTAG	GAGCTGCAGT	CACGTAATCG	2250
AGGTGGCAAG	ATGTCCTCTA	AAGATGTAGG	GAAAAGTGAG	AGAGGGGTGA	2300
GGGTGTGGGG	CTCCGGGTGA	GAGTGGTGGA	GTGTCAATGC	CCTGAGCTGG	2350
GGCATTTTGG	GCTTTGGGAA	ACTGCAGTTC	CTTCTGGGGG	AGCTGATTGT	2400
AATGATCTTG	GGTGGATCC				2419

- (2) INFORMATION FOR SEQUENCE ID NO: 8:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5674 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single

 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-1 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CCCGGGGCAC	CACTGGCATC	CCTCCCCCTA	CCACCCCAA	TCCCTCCCTT	50
TACGCCACCC	ATCCAAACAT	CTTCACGCTC	ACCCCCAGCC	CAAGCCAGGC	100
AGAATCCGGT	TCCACCCCTG	CTCTCAACCC	AGGGAAGCCC	AGGTGCCCAG	150
ATGTGACGCC	ACTGACTTGA	GCATTAGTGG	TTAGAGAGAA	GCGAGGTTTT	200
CGGTCTGAGG	GGCGGCTTGA	GATCGGTGGA	GGGAAGCGGG	CCCAGCTCTG	250
TAAGGAGGCA	AGGTGACATG	CTGAGGGAGG	ACTGAGGACC	CACTTACCCC	300
AGATAGA GGA	CCCCAAATAA	TCCCTTCATG	CCAGTCCTGG	ACCATCTGGT	350
GGTGGACTTC	TCAGGCTGGG	CCACCCCAG	CCCCCTTGCT	GCTTAAACCA	400
CTGGGGACTC	GAAGTCAGAG	CTCCGTGTGA	TCAGGGAAGG	GCTGCTTAGG	450
AGAGGCAGC	GTCCAGGCTC	TGCCAGACAT	CATGCTCAGG	ATTCTCAAGG	500
AGGGCTGAGG	GTCCCTAAGA	CCCCACTCCC	GTGACCCAAC	CCCCACTCCA	550
ATGCTCACTC	CCGTGACCCA	ACCCCCTCTT	CATTGTCATT	CCAACCCCCA	600
CCCCACATCC	CCCACCCCAT	CCCTCAACCC	TGATGCCCAT	CCGCCCAGCC	650
ATTCCACCCT	CACCCCCACC	CCCACCCCCA	CGCCCACTCC	CACCCCCACC	700
CAGGCAGGAT	CCGGTTCCCG	CCAGGAAACA	TCCGGGTGCC	CGGATGTGAC	750
GCCACTGACT	TGCGCATTGT	GGGGCAGAGA	GAAGCGAGGT	TTCCATTCTG	800

AGGGACGGCG	TAGAGTTCGG	CCGAAGGAAC	CTGACCCAGG	CTCTGTGAGG	850
	AGAGGCTGAG				900
	AATATTCCAG				950
	CGTCTCAGCC			·	1000
	CACCAGGTTC				1050
	GCAGGACTGG				1100
	TCAGCACCCA				1150
	CCACTCCCAC				1200
	CAGCTACACC				1250
	ACCCTCCAGC				1300
	TGCCCCCAAC				1350
	CCCCCATTCT				1400
	CCTGGTAGGC				1450
	GAAGCCAGGT				1500
	GGGAGTGGTT				1550
-	ACTGAGGAGG				1600
	ACCCCTGCTG				1650
	GACCACCCC				1700
	AGTCATAGCT				1750
	AGGCATCAAG				1800
	GGAACTGAGG				1850
	CCACTCACAT				1900
	ATCCCTGCTG				1950
	GATCTTGACG				2000
	GGCCTCAGGG				2050
	AGAGGACCCA				2100
	CCACTTCTGG				2150
	GTGGGACCCA				2200
	AGGGGACCTT				2250
	GGGCACGGTG				2300
	GGACAGAGCT				2350
	GTTCCAGGAT				2400
	ATATCCCCGG				2450
	TTAGTAGCTC				2500
	ACTTGTACCA				2550
	GGGGTAAAGG				2600
	GCACAGGCGC				2650
	AATCCACACC				2700
	TGTGGCTTCT				2750
	CATTCTCAGA				2800
	AGACAGAGCG				2850
	GAGGACTGAG				2900
	ATCAGCCCTG				2950
	CCGAGGTCCT				3000
	CTTGGTCTGA				3050
	CTGCCAGGAG				3100
	TAATTCCAAT				3150
	GCACGTGTGG				3200
	GGATGTGAAC				3250
	CAGGCCCTGC				3300
	CATCCACTGC				3350
	GTAGCACTGA				3400
CACCCTCCTG	GIAGCACIGA	DDDAJJDAAD	CIGIGCIIGC	GGICIGCACC	3400

CTGAGGGCCC GTGGATTCCT CTTCCTGGAG CTCCAGGAAC (CAGGCAGTGA	3450
GGCCTTGGTC TGAGACAGTA TCCTCAGGTC ACAGAGCAGA		3500
GGTGTGCCAG CAGTGAATGT TTGCCCTGAA TGCACACCAA		3550
TGCCACAGGA CACATAGGAC TCCACAGAGT CTGGCCTCAC C		3600
TCAGTCCTGT AGAATCGACC TCTGCTGGCC GGCTGTACCC T		3650
CTCACTTCCT CCTTCAGGTT TTCAGGGGAC AGGCCAACCC A		3700
ATTCCCTGGA GGCCACAGAG GAGCACCAAG GAGAAGATCT G	GTAAGTAGGC	3750
CTTTGTTAGA GTCTCCAAGG TTCAGTTCTC AGCTGAGGCC T		3800
TCCCTCTCTC CCCAGGCCTG TGGGTCTTCA TTGCCCAGCT C		3850
CTCCTGCCTG CTGCCCTGAC GAGAGTCATC		3880
ATG TCT CTT GAG CAG AGG AGT CTG CAC TGC AAG C	CCT GAG GAA	3922
GCC CTT GAG GCC CAA CAA GAG GCC CTG GGC CTG		3964
CAG GCT GCC ACC TCC TCC TCC TCT CCT CTG GTC C		4006
CTG GAG GAG GTG CCC ACT GCT GGG TCA ACA GAT C		4048
AGT CCT CAG GGA GCC TCC GCC TTT CCC ACT ACC A		4090
ACT CGA CAG AGG CAA CCC AGT GAG GGT TCC AGC A		4132
GAG GAG GGG CCA AGC ACC TCT TGT ATC CTG GAG T		4184
CGA GCA GTA ATC ACT AAG AAG GTG GCT GAT TTG		4216
CTG CTC CTC AAA TAT CGA GCC AGG GAG CCA GTC A		4258
GAA ATG CTG GAG AGT GTC ATC AAA AAT TAC AAG C		4300
CCT GAG ATC TTC GGC AAA GCC TCT GAG TCC TTG C		4342
TTT GGC ATT GAC GTG AAG GAA GCA GAC CCC ACC G	GGC CAC TCC	4384
TAT GTC CTT GTC ACC TGC CTA GGT CTC TCC TAT G	GAT GGC CTG	4426
CTG GGT GAT AAT CAG ATC ATG CCC AAG ACA GGC T		4468
ATT GTC CTG GTC ATG ATT GCA ATG GAG GGC GGC C	CAT GCT CCT	4510
GAG GAG GAA ATC TGG GAG GAG CTG AGT GTG ATG		4552
GAT GGG AGG GAG CAC AGT GCC TAT GGG GAG CCC A	AGG AAG CTG	4594
CTC ACC CAA GAT TTG GTG CAG GAA AAG TAC CTG	GAG TAC GGC	4636
AGG TGC CGG ACA GTG ATC CCG CAC GCT ATG AGT T	TCC TGT GGG	4688
GTC CAA GGG CCC TCG CTG AAA CCA GCT ATG TGA		4711
AAGTCCTTGA GTATGTGATC AAGGTCAGTG CAAGAGTTC		4750
GCTTTTTCTT CCCATCCCTG CGTGAAGCAG CTTTGAGAGA	GGAGGAAGAG	4800
GGAGTCTGAG CATGAGTTGC AGCCAAGGCC AGTGGGAGGG G		4850
AGTGCACCTT CCAGGGCCGC GTCCAGCAGC TTCCCCTGCC T	TCGTGTGACA	4900
TGAGGCCCAT TCTTCACTCT GAAGAGAGCG GTCAGTGTTC T	TCAGTAGTAG	4950
GTTTCTGTTC TATTGGGTGA CTTGGAGATT TATCTTTGTT C	CTCTTTGGA	5000
ATTGTTCAAA TGTTTTTTTT TAAGGGATGG TTGAATGAAC T	TTCAGCATCC	5050
AAGTTTATGA ATGACAGCAG TCACACAGTT CTGTGTATAT A	AGTTTAAGGG	5100
TAAGAGTCTT GTGTTTTATT CAGATTGGGA AATCCATTCT A		5150
TTGGGATAAT AACAGCAGTG GAATAAGTAC TTAGAAATGT G	GAAAAATGAG	5200
CAGTAAAATA GATGAGATAA AGAACTAAAG AAATTAAGAG A	ATAGTCAATT	5250
CTTGCCTTAT ACCTCAGTCT ATTCTGTAAA ATTTTTAAAG A	ATATATGCAT	5300
ACCTGGATTT CCTTGGCTTC TTTGAGAATG TAAGAGAAAT T		5350
TAAAGAATTC TTCCTGTTCA CTGGCTCTTT TCTTCTCCAT G		5400
TCTGCTTTTT GGAAGGCCCT GGGTTAGTAG TGGAGATGCT A	AAGGTAAGCC	5450
AGACTCATAC CCACCCATAG GGTCGTAGAG TCTAGGAGCT		5500
AATCGAGGTG GCAAGATGTC CTCTAAAGAT GTAGGGAAAA G		5550
GGTGAGGGTG TGGGGCTCCG GGTGAGAGTG GTGGAGTGTC		5600
GCTGGGGCAT TTTGGGCTTT GGGAAACTGC AGTTCCTTCT C	GGGGAGCTG	5650
ATTGTAATGA TCTTGGGTGG ATCC		5674



- (2) INFORMATION FOR SEQUENCE ID NO: 9:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4157 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: genomic DNA
 - (ix) FEATURE:
 - (A) NAME/KEY: MAGE-2 gene
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

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	TCCCCATCCG				50
	TCACGGGCCC				100
	CAGCGAGATT				150
	GGCGCAGGCT				200
	CGGGCCTCAC				250
	CTGCCGGGCC				300
	CACCACCTCA				350
	CGTAAGAGCT				400
	CCAGACTCAG				450
	AACCCACCCC	<del>-</del>			500
	CCCCCATCCC				550
TCCCATCTCC	TCCCCCACCA	CCATCCTGGC	AGAATCCGGC	TTTGCCCCTG	600
CAATCAACCC	ACGGAAGCTC	CGGGAATGGC	GGCCAAGCAC	GCGGATCCTG	650
	GTACGGCTAA				700
GGCCTTTGGG	ATGCAGAGGA	AGGGCCCAGG	CCTCCTGGAA	GACAGTGGAG	750
TCCTTAGGGG	ACCCAGCATG	CCAGGACAGG	GGGCCCACTG	TACCCCTGTC	800
TCAAACTGAG	CCACCTTTTC	ATTCAGCCGA	GGGAATCCTA	GGGATGCAGA	850
CCCACTTCAG	GGGGTTGGGG	CCCAGCCTGC	GAGGAGTCAA	GGGGAGGAAG	900
<b>AAGAGGG</b> AGG	ACTGAGGGGA	CCTTGGAGTC	CAGATCAGTG	GCAACCTTGG	950
GCTGGGGGAT	CCTGGGCACA	GTGGCCGAAT	GTGCCCCGTG	CTCATTGCAC	1000
CTTCAGGGTG	ACAGAGAGTT	GAGGGCTGTG	GTCTGAGGGC	TGGGACTTCA	1050
GGTCAGCAGA	GGGAGGAATC	CCAGGATCTG	CCGGACCCAA	GGTGTGCCCC	1100
CTTCATGAGG	ACTCCCCATA	CCCCCGGCCC	AGAAAGAAGG	GATGCCACAG	1150
AGTCTGGAAG	TAAATTGTTC	TTAGCTCTGG	GGGAACCTGA	TCAGGGATGG	1200
CCCTAAGTGA	CAATCTCATT	TGTACCACAG	GCAGGAGGTT	GGGGAACCCT	1250
CAGGGAGATA	AGGTGTTGGT	GTAAAGAGGA	GCTGTCTGCT	CATTTCAGGG	1300
GGTTCCCCCT	TGAGAAAGGG	CAGTCCCTGG	CAGGAGTAAA	GATGAGTAAC	1350
CCACAGGAGG	CCATCATAAC	GTTCACCCTA	GAACCAAAGG	GGTCAGCCCT	1400
GGACAACGCA	CGTGGGGTAA	CAGGATGTGG	CCCCTCCTCA	CTTGTCTTTC	1450
CAGATCTCAG	GGAGTTGATG	ACCTTGTTTT	CAGAAGGTGA	CTCAGTCAAC	1500
ACAGGGGCCC	CTCTGGTCGA	CAGATGCAGT	GGTTCTAGGA	TCTGCCAAGC	1550
	AGAGCCTGAG				1600
	GGCCCCATAG				1650
	CAGGGCTGTC				1700
	GAAGGGGAGG				1750
	GGTCTCAGGC				1800
	CCAGGACACC				1850
	GAGGACCTGG				1900
	TACCATATCA				1950

CAAGCCAGCA         AAAGGGTGGG         ATTAGGCCCT         ACAAGTAGAGA         AGGTGAGGGC         2000           CCTGAGTGGG         CCAACCCTGC         TEAAGTACCT         GGGAGTCTGG         2000           GCAGTCTGG         CCAACCCTGC         TEAAGACTTCT         GGGATCTGG         2150           TCCAGGAACC         AGGCAGTGAG         CCTCTCCCCAG         AATCAGGACC         2200           AGAGCACAGG         GCCCACCACAGC         AGTGCAACA         ATTGGGACTC         CACACCAGAG         GCCTCACCCT         CCCTGAACAA         ATTGGGACTC         CACACCAGAG         2250           CACACCAGAG         GCCTCACCCT         CACTTCCTCAGCT         CACTTCCAGCT         CACTTCCAGCTC         CACTTCCAGCT         CACTTCCAGCTC         CACTTCCAGGCTC         CACTTCCAGGCTC         CACTTCCAGGCTC         CACTTCCAGGCTC         CACTTCCAGGCTC         CACTTCCAGGCTC         CACTTCCAGGCTC         CACTTCCAGGCTC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCTCC         CACTTCCAGGCCACCC         CACTTCCACCCACCCACCCC         CACTTCCACCCACCCACCCC         CACTTCCACCCACCCC         CACTTCCACCCACCCC         CACTTCCACCCACCCC         CACTTCCACCCACCCCCCCCCCCCCCCCCCCCCCCCCC	CARCOCACOA ARROCCOMOCO AMBROCCOCO A	03.3.003.03.3. 3.00M03.0000	
GGGAGTCTGG         CCAACCCTGC         TGGAGATCCTC         GGCTGTGCTT         210           GCAGTCTGCA         ACATGAAGGC         CCTGTCCAGGA         AATCAGGAGC         2150           TCCAGGAACA         AGGCAGTAGA         CCTTGTCTC         GATCAGGAGC         2200           AGAGCAGAGG         GGCACCCCC         CCCAGACCAA         ATGGACTCTC         CACACCAGAG         2250           CACACCAGAG         GCCCACCCC         CCCAGACCAA         ATGGGACTCC         CAGCGCTCC         2300           GCCTGACCCT         CCCCAGACCAA         ATGGGACCCC         AGGCGTCCT         CTGTACCCTG         CAGGCTCCT         CAGGCTCCT         CAGGCTCCT         CAGGCTCCT         CTGTAAGTAA         AGGACACATGA         AGGAGACATTCA         AGGAGAACAT         2450           AGGCTGACAA         AGGCCTCCAA         AGGCCTCCAA         AGGCCTCCAA         AGGACACCCCA         AGGCCTCAA         AGGACACCCCA         AGCCTCAACCACACACACCCCACCCACCACCACCACCACCAC			
GCAGTCTECA         ACTGARAGGC         CCTGTGCATTC         CTCTCAGGTACC         2150           TCCAGGAACC         AGCCAGGAGC         AGTGCCAACA         CTCAGGTCAC         2200           AGAGCAGAGG         GACTGCACCA         AGTGCCAACA         CTGAAGGTTT         GCCTGACCCG         2250           GCCTCACCCC         CCCAGAACA         ATGGGACTC         AGAGGCCTG         2350           GCCTCACCCT         CCCTATTCTC         CACTGCAGT         TGCGGGGCCCT         2350           CTGTAACCTA         AGGGGCCCT         CCACTTCCCC         CTGGAGGAC         2400           AGGCTGACAA         GAGGGCCCC         CACCTCCAA         GGTCCACTCCCC         2500           CTGTAAGTAA         GAGGCCCC         AGGCCTCCAA         GGTCTCACCCCACC         2500           CAGAGGCCCA         AGGCACTGCA         GGTCACTCACCACCCCCACC         CTCCCCCACCTCCC         2500           CCCAGCTCCT         GCCCTGCCACCCTCCCCCACCCC         CCCCACCTCCCTC         AGCCCTTCACCACCACCCCACCC         2500           ATG         CCCACCTCCTC         AGCCCTCCACCACCCACCCCCACCCCCCCCCCCCCCCCC	CCTGAGTGAG CACAGAGGGG ACCCTCCACC CA	AAGTAGAGT GGGGACCTCA 20!	50
TCCAGGAACC         AGGCAGTGGG         CCCTTGGTCT         GATCAGTGC         2250           CAGACCAAGG         GAGCCCACCCG         CCCAGACAAA         ATTGGGACTC         AGAGGGCCTG         2300           GCCTCACCCT         CCCTATTCTC         AGTCCTGCAG         CCTGAGCCT         CAGGGGGCCT         2350           CTGTACCCT         AGGCCCCACCCACCTCCTC         CCTGAGGGGAC         2400           AGGCTGACAA         GTAGGGGCTC         CCCACTTCCTC         CTCTAGGGGAC         2400           AGGCTGACAA         GTAGGACCCC         AGGCCTCCAA         AGTCTACACC         2500           CTGTAAGTAA         GCCTTGTCA         AGGCCTCCAA         GTTCTCATCC         2500           CAAGGCTCC         CTCCCCCAAGCTCC         TTCTCCCCC         AGGCTACCAC         AGTCATC         2550           CCCAGCTCCT         CTCCTCCCC         AGGCTACCAC         AGTCATC         2577         AGTCACCCC         260         261         262         263         263         263         263         263         263         263         263         262         263         263         262         264         264         267         267         260         267         267         267         262         266         262         267         262	CGGAGTCTGG CCAACCCTGC TGAGACTTCT GO	GGAATCCGT GGCTGTGCTT 210	00
TCCAGGAACC         AGGCAGTGGAC         AGTCCAACA         CTGAGGTCAC         2250           CACACCAAGG         GACGCCACCC         CCCAGACAAA         ATGGGACTC         AGAGGGCTG         2300           GCCTCACCCT         CCCTATTCTC         AGTCCCACAAC         CTGAGCCTC         CAGAGGGACC         2350           CTGTACCCT         AGTCGTCCACCC         CCCACTTCCTC         CTTCAGGGGAC         2400           AGGCTGACAA         GTAGGGCTC         CACACTCCT         CTTCAGGTTC         TTGAGGGGAC         2400           AGGCTCACAA         GTAGGACCCC         AGGCCTCCAA         GGTTCAGTTC         AGTCTCACC         2500           AGGCTAGAA         GTAGGACCTCC         CTCACCCCACCTC         CTCTCACC         AGGCTTCACCC         2500           CCCAGCTCCT         CTCCTCCCC         AGGCTTCACAC         AGTCATC         2550           CCCAGCTCCT         CTCCTCCCC         AGGCTACCAC         AGTCATC         257           ATG         CTT         AGC         AGC         AGTCATC         263         263           AGG         CTT         GCC         CAC         AGC         AGC         AGC         AGC         264         267         262         266         262         267         262         262         262	GCAGTCTGCA CACTGAAGGC CCGTGCATTC CT	CTCCCAGG AATCAGGAGC 21!	50
AGAGCAGAGG GGACCCACCC CCCAGAACAA ATGAGCATT GCCTGGAATG CACACCAGG GCCCCACCCC CCCAGAACAA ATGAGACTC AGAGGGCCTG GCCTCACCCT CCCTATTCTC AGTCCTGCAG CTGACCATG GCCTCACCCT CCCTATTCTC AGTCCTGCAG CTGACCATG GCCTCACCCT CCCTATTCTC CTTCAGGTTC TGAGGAGACAT AGGCGCACAA GTAGCACCCC AGGCACTGGA GGAGCATTGA AGGAGAACAT CAGGCCTCAA GTAGCACCCA AGGCCACTGGA GGAGCATTGA AGGAGAACAT CACACCCCACCTCC TTCTCTCCCC AGGCCTGTGA GTCATCACC CCCAGGTCCA CACACGCCTC TTCTCTCCCC AGGCCTGTGA GTCATCATTG CCCAGGTCCT GCCCGCACTC CTGCCTGCTG GCCTGACCAA GTTCATTG CCCAGGTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAA GATCATC CCCAGGTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAA GATCATC CCCAGGTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAA GATCATC AGC CT CTT GAG GCA GAG AGG AGC CAC TGC AAG CCT GAA GAA CAG CCT CTT GAG GCC CGA GGA GAG CAC CAC AGC CTG GTG GTG GC CAG CTC CTT GAG GCC CGA GAG GAG CAC GAC ACC GCT TCT TCC TCT CAT ACT CTA GTG GAA GTT ACC CTG GGG GAG GTG CCT GAC GCC CAC CCG AGC CCC CAC AGT CCT CAG GGA GCC TCC AGC CAC CAC ACC ACC ACC CAC AGT CCT CAG GGA GCC TCC AGC CAC CAC ACC AAC AAC AAC AAC AAC AAC ACA CAA AAC TTC CTT TGG AGA CAA TCC GAT CCC GAC CTG GAG TCC CAC AGC ACC AAC AAT TCT CCC GAC CTG GAG TCC CAC AGC ACC AAC AAT ACC ATC ATT AGC CCC GAC CTG GAG TCC CAC AGC AAC CAA AAC GAC GAC ATC AGT AGC AAC AAG GCC TCC AGC CAC GAG ACC CAA GAA GAG GAG GGG CCA AGA ATT TT AGA AAT TGC CAG GAC TTC CTT TT CCT CAAC TATC CAT AGC ACC CCG GAC CTG GAG TCC CAC GAC AAC GAA ATC GTT AGG AAC CCG GAG TAC TTG CAC AAC GAA GAA ATG CTTC AGC AAC CAG AAC AGC CAC AAC GAA AAC GAC GAC ATC AGT AGC ACC CAG GAC TCC TTC TCT TTT CCC CTC AAC TATC CTC CAG AAC ACC AGC CAC TTC TTT GCC ATC GAC GTC GTC CAC ACC AAC ACC AAC GAA AAC GAC GAC ATC AGT AGC AAC CCC GAC TAC ATG CAC AAC GAC AAC GAC ATC ATC GTC CCC GAC TAC AAC GAC CTC TTT TC CCC TC AAC TATC CTC CAC GAC TAC CAC AAC GCC CCT TTT GCC ACC CTC CCC TCC CAC GAC TAC CTC CAC AAC CAC CCC CTC CAC GCC CCC AAC ACC ACC CCC CTC CAC GAC AAC CAC CCC CCC AAC ACC ACC CCC CCC C			
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GCCTCACCCT CCCTATTCTC AGTCCTGCAG CCTGAGCATG TGCTGGCGGG CTGTACCCTG AGGTGCCCTC CCACTTCCTC CTTCAGGTTC TGAGGGGGAC AGGTGACAA GTAGGACCCG AGGCACTGGA GGAGCATTGA AGGAGAGAGAT AGGAGTACAA GTAGGACCCG AGGCACTGCA GGAGCATTGA AGGAGAAGAT CTGTAAGTAA GCCTTTGTCA GAGCCTCCAA GGTTCATTC AGTTCTACC CTAGAGCCTCA CACACGCTCC TTCTCTCCCCC AGGCCTGTGG GTCTTCATTG CCCAGCTCCT GCCCGCACTC CTGCCTGCTG CCCTGACCAG AGTCATT ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA AGGAGGACTA CACACGCTCC TTCCTCTCCCC AGGCCTGTAGCAGA AGTCATC ATG CCT CTT GAG CAC CAG AGG AGG CCC CTG GGC CTG GGT GGT GGC CCCAGCTCCT GAG CAC CAC AGG AGG CCC CTG GGC CTG GGT GGT GCG AGG CTC TAGG CAC CAC AGG AGG CCC CTG GGC CTG GGT GGT CCC GAC CTC ACT GAG GAG CAC CAG ACC CCT TCT TCC TCT CTA ACT CTA GTG GAA GTT ACC CTG GGG GAG GTC CCT GCC CAC CCG AGT CCT CCC CAC AGT CCT CAG GGA GCC TCC AGC CAC CTG ACT ACC ATC AAC CAC ACT CTT TGG AGA CAA TCC GAT CTC TCT GAG CCC AAC CAA GAA GAG GAG GCC CTC AGC CAC CTG GAG TCC CAC AGG AGG GGC CCA AGA ATC CAT CCC GAC CTG GAG TCC CAC AGGA GAG GGC CCA AGA ATC CAT CCC GAC CTG GAG TCC CAC AGGA GAG GGC CCA AGA ATC TTT CCC GAC CTG GAG TCC CAC AGA GAA GAG GGC CCA AGA ATC AGT TACT CAG CCC CTC AGG CAC ACC AGA CTG GAG TTC CAA GCA GCA ATC AGT AGG AGG AGG TTC CAC AAC CAA GAA AGC GGA ATC AGT AGG AGC CCG GAC CTG GAG CTC CTT TTT CCC GTG ATC TTC AGC AAC CCC CAG CCC GAC CTC CTG CTG GCC CTC GAG GTG GCC CAC CTG GAG CTC CTC ACA AAC CAC GCA ATC CAC AGA CAC GCC GCC TCC TTG TTC CTC CAC GAG GTG CTC CAC AGA CAC GCC CTC TTT TTT CCC CTC GAG GAT GTC CTC CAG TAC TTG CAC CAC TTG TAC ATC CTT GTC ACC TGC GAA ACC TTC CTA AGC CAC TTG TAC ATC CTT GTC ACC TGC GAA CCC CAG CAC CTC CTG ATA ATC GTC CTC GCC CAG ACA CGC CTC CTG ATA ATC GTC CTC GCC AGA ACA GCC CTC CTG ATA ATC GTC CTG GCC AGA CAC GCC CTC TGT ATA ATC GTC CTC GCC AGA ACC TCC CAG AAC CTC CTG AGA GAG GAG GAC AGT CTC CTG GAT ATG TTG GAG CTC CTC ATG GAC AAA ATC CTG GTC CATC CAC CAC CTC CTG ATA ATC GTC CTC GTG GAG GAG CTC TCC CAC AGG AC CTC CTG TGG GGC CAC ATC TTT GAA GAC CAC TCC CTA GAG GCC CTC CTG TGG GGC CAC ATC CTC GGC CAC TTC TTT GAA CCC			
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CAG GCT         CCT         GCT         ACT         GAG         CAG         CAG         GCT         TCT         TCT         TCT         2723           TCT         ACT         AGT         GAT         ACC         CTG         GCC         2765           GAC         TCA         AGT         AGT         CCC         CAC         AGT         CCT         GAG         2807           TTC         TCG         ACC         AAC         AAC         TAC         ACT         CCT         CAG         AAC         CAA         GAA         GAA         GAA         GAA         GAA         CAA         GAA         GAA         GAA         CAA         AGA         AAA         GAA         GAA         AGA         AGA <td></td> <td>·</td> <td></td>		·	
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ATG GTT GAG TTG GTT CAT TTT CTG CTC CTC AAG TAT CGA GCC  AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC  AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC  30.17  AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC  30.59  TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTG GAA  GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG  31.43  GGC CTC TCC TAC GAT GGC CTG CTG GGC GAC AAT CAG GTC ATG  ATA GAG GGC CTC CTG ATA ATC GTC CTG GCC ATA ATC GCA  ATA GAG GGC CTC TGT GCC CCT GAG GAG AAA ATC GGC GAG GAG  CTG AGT ATG TTG GAG GTG TTT GAG GGG AGG GAG GA	GAG GGC TCC AGC AAC CAA GAA GAG GAC	G GGG CCA AGA ATG TTT 289	91
AGG GAG CCG GTC ACA AAG GCA GAA ATG CTG GAG AGT GTC CTC  AGA AAT TGC CAG GAC TTC TTT CCC GTG ATC TTC AGC AAA GCC  3059 TCC GAG TAC TTG CAG CTG GTC TTT GGC ATC GAG GTG GTA GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GTG GTC CCC ATC AGC CAC TTG TAC ATC CTT GTC ACC TGC CTG GGC CTC TCC TAC GAT GGC CTG GTG GTG GAA AAT CAG GTC ATG GGC CTC TCC TAC GAT GGC CTG GTG GTG GAC AAT CAG GTC ATG AGA GAC GGC CTC CTG ATA ATC GTC CTG GGC ATA ATC GCA ATA GAG GGC GAC TGT GCC CCT GAG GAG AAA ATC TGG GAG GAG ATA ATC GCA ATA GAG GGC GAC TGT GAC GTG GTG GTG GAG GAG AAA ATC ATG TAG GAG GTG TTT GAG GGG AGA AAA ATC ATG GAG GAG GAG AAA ATC ATG TAG GAG GTG TTT GAG GGG AGA GAC AAT ATC GCA CAT CCC AGG AAG CTG CTC ATG CAA GAT GTC ATT GAG GAG TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT ACC AGC TAT GTG GAG TAC CGG CAG GTG CCC GGC AGT GAT ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT ATT GAA GAG GAG GAA GAG TGC AGC GAA GAG GAG GAA GAG TGC ACC ATC CAC ATT TCC TAC CAC CCC CTG CAT GAA CGG GCT ATT GAA GAG GAG GAA GAG TGA ACC AGC TAT GTG GAA GAG TGA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT ATT GAA GAG GAG GAA GAG TGA ATTTCTTCAGCAC ATTTTCC TAC CAC CCC CTG CAT GAA CGG GCT AGCACTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG AGCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG AGCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG AGCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG AGCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG AGCACCATAGAA TTTTTTTAT CAGAATGGT TACTTTTTTT CCTGACAA ATGTTTGAAA GACACATAGGT CACACATAGGT CACCATACACATACA GTCCCAAA ATACACGAG TGGAATAGT TATTTTTTTT CAGCAGTAGA ATACACGAG TGGAATAGT TATTTTTTTTT CAGCATTATATAAA TATTTTTTTTTT	CCC GAC CTG GAG TCC GAG TTC CAA GCA	A GCA ATC AGT AGG AAG 293	33
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GAA AAC TAC CTG GAG TAC CGG CAG GTG CCC GGC AGT GAT CCT GCA TGC TAC GAG TTC CTG TGG GGT CCA AGG GCC CTC ATT GAA ACC AGC TAT GTG AAA GTC CTG CAC CAT ACA CTA AAG ATC GGT GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842 TAAGAGTCCT GTTTTTTATT CAGATTGGA AATCCATTCC ATTTTGTGAG TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAAGAT AGTTAATTCT TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCT TGTGGAAGGC	CTG AGT ATG TTG GAG GTG TTT GAG GGC	G AGG GAG GAC AGT GTC 331	11
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GGA GAA CCT CAC ATT TCC TAC CCA CCC CTG CAT GAA CGG GCT TTG AGA GAG GGA GAA GAG TGA GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG TAAGAGTCCT GTTTTTATT CAGATTGGA AATCCATTCC ATTTTGTGAG TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TCCCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCT TGTGGAAGGC			
TTG AGA GAG GGA GAA GAG TGA  GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT  GCACCTTCCA GGGCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA  GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG  TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA  TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA  GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG  TAAGAGGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG  TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG  AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAAGAT AGTTAATTCT  TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT  4042  TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCT TGTGGAAGGC  4142			
GTCTCAGCAC ATGTTGCAGC CAGGGCCAGT GGGAGGGGGT CTGGGCCAGT GCACCTTCCA GGGCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA GGCCCATTCC TGCCTCTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAAATATG TGTATGTTTT TGCCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCT TGTGGAAGGC 4142			
GCACCTTCCA GGGCCCCATC CATTAGCTTC CACTGCCTCG TGTGATATGA 3642 GGCCCATTCC TGCCTCTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842 TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG 3942 AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC			
GGCCCATTCC TGCCTCTTTG AAGAGAGCAG TCAGCATTCT TAGCAGTGAG 3692 TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842 TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG 3942 AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC			
TTTCTGTTCT GTTGGATGAC TTTGAGATTT ATCTTTCTTT CCTGTTGGAA 3742 TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842 TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG 3942 AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142			
TTGTTCAAAT GTTCCTTTTA ACAAATGGTT GGATGAACTT CAGCATCCAA 3792 GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842 TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142			
GTTTATGAAT GACAGTAGTC ACACATAGTG CTGTTTATAT AGTTTAGGGG 3842 TAAGAGTCCT GTTTTTATT CAGATTGGGA AATCCATTCC ATTTTGTGAG 3892 TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142			
TAAGAGTCCTGTTTTTTATTCAGATTGGGAAATCCATTCCATTTTGTGAG3892TTGTCACATAATAACAGCAGTGGAATATGTATTTGCCTATATTGTGAACG3942AATTAGCAGTAAAATACATGATACAAGGAACTCAAAAGATAGTTAATTCT3992TGCCTTATACCTCAGTCTATTATGTAAAATTAAAAATATGTGTATGTTTT4042TGCTTCTTTGAGAATGCAAAAGAAATTAAATCTGAATAAATTCTTCCTGT4092TCACTGGCTCATTTCTTTACCATTCACTCAGCATCTGCTCTGTGGAAGGC4142			92
TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142	GTTTATGAAT GACAGTAGTC ACACATAGTG CT	GTTTATAT AGTTTAGGGG 384	12
TTGTCACATA ATAACAGCAG TGGAATATGT ATTTGCCTAT ATTGTGAACG AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142			92
AATTAGCAGT AAAATACATG ATACAAGGAA CTCAAAAGAT AGTTAATTCT 3992 TGCCTTATAC CTCAGTCTAT TATGTAAAAT TAAAAATATG TGTATGTTTT 4042 TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142			
TGCCTTATACCTCAGTCTATTATGTAAAATTAAAAATATGTGTATGTTTT4042TGCTTCTTTGAGAATGCAAAAGAAATTAAATCTGAATAAATTCTTCCTGT4092TCACTGGCTCATTTCTTTACCATTCACTCAGCATCTGCTCTGTGGAAGGC4142			
TGCTTCTTTG AGAATGCAAA AGAAATTAAA TCTGAATAAA TTCTTCCTGT 4092 TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142			
TCACTGGCTC ATTTCTTTAC CATTCACTCA GCATCTGCTC TGTGGAAGGC 4142			
CCTGGTAGTA GTGGG 4157			
	CCTGGTAGTA GTGGG	419	<i>ا</i> د

- (2) INFORMATION FOR SEQUENCE ID NO: 10:
   (i) SEQUENCE CHARACTERISTICS:
   (A) LENGTH: 662 base pairs
   (B) TYPE: nucleic acid
   (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-21 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

GGATCCCCAT	GGATCCAGGA	AGAATCCAGT	TCCACCCCTG	CTGTGAACCC	50
<b>AGGGAA</b> GTCA	CGGGGCCGGA	TGTGACGCCA	CTGACTTGCG	CGTTGGAGGT	100
CAGAGAACAG	CGAGATTCTC	GCCCTGAGCA	ACGGCCTGAC	GTCGGCGGAG	150
GGAAGCAGGC	GCAGGCTCCG	TGAGGAGGCA	AGGTAAGATG	CCGAGGGAGG	200
ACTGAGGCGG	GCCTCACCCC	AGACAGAGGG	CCCCCAATAA	TCCAGCGCTG	250
CCTCTGCTGC	CAGGCCTGGA	CCACCCTGCA	GGGGAAGACT	TCTCAGGCTC	300
AGTCGCCACC	ACCTCACCCC	GCCACCCCC	GCCGCTTTAA	CCGCAGGGAA	350
CTCTGGTGTA	AGAGCTTTGT	GTGACCAGGG	CAGGGCTGGT	TAGAAGTGCT	400
CAGGGCCCAG	ACTCAGCCAG	GAATCAAGGT	CAGGACCCCA	AGAGGGGACT	450
GAGGGTAACC	CCCCCGCACC	CCCACCACCA	TTCCCATCCC	CCAACACCAA	500
CCCCACCCC	ATCCCCCAAC	ACCAAACCCA	CCACCATCGC	TCAAACATCA	550
ACGGCACCCC	CAAACCCCGA	TTCCCATCCC	CACCCATCCT	GGCAGAATCG	600
GAGCTTTGCC	CCTGCAATCA	ACCCACGGAA	GCTCCGGGAA	TGGCGGCCAA	650
GCACGCGGAT	CC				662

- (2) INFORMATION FOR SEQUENCE ID NO: 11:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1640 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (ix) FEATURE:
    - (A) NAME/KEY: cDNA MAGE-3
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GCCGCGAGGG AAGCCGGCCC AGGCTCGGTG AGGAGGCAAG GTTCTGAGGG	50
GACAGGCTGA CCTGGAGGAC CAGAGGCCCC CGGAGGAGCA CTGAAGGAGA	100
AGATCTGCCA GTGGGTCTCC ATTGCCCAGC TCCTGCCCAC ACTCCCGCCT	150
GTTGCCCTGA CCAGAGTCAT C	171
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT GAA GAA	213
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG GGT GCG	255
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC TCT	297
TCT ACT CTA GTT GAA GTC ACC CTG GGG GAG GTG CCT GCC	339
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC TCC AGC	381
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA TCC TAT	423

GAG (	GAC	TCC	AGC	AAC	CAA	GAA	GAG	GAG	GGG	CCA	AGC	ACC	TTC	465
CCT (	GAC	CTG	GAG	TCC	GAG	TTC	CAA	GCA	GCA	CTC	AGT	AGG	AAG	507
GTG (	GCC	GAG	TTG	GTT	CAT	TTT	CTG	CTC	CTC	AAG	TAT	CGA	GCC	549
AGG (	GAG	CCG	GTC	ACA	AAG	GCA	GAA	ATG	CTG	GGG	AGT	GTC	GTC	591
GGA 2	AAT	TGG	CAG	TAT	TTC	TTT	CCT	GTG	ATC	TTC	AGC	AAA	GCT	633
TCC Z	AGT	TCC	TTG	CAG	CTG	GTC	TTT	GGC	ATC	GAG	CTG	ATG	GAA	675
GTG (	GAC	CCC	ATC	GGC	CAC	TTG	TAC	ATC	TTT	GCC	ACC	TGC	CTG	717
GGC (	CTC	TCC	TAC	GAT	GGC	CTG	CTG	GGT	GAC	AAT	CAG	ATC	ATG	759
CCC 2	AAG	GCA	GGC	CTC	CTG	ATA	ATC	GTC	CTG	GCC	ATA	ATC	GCA	801
AGA (	GAG	GGC	GAC	TGT	GCC	CCT	GAG	GAG	AAA	ATC	TGG	GAG	GAG	843
CTG Z	AGT	GTG	TTA	GAG	GTG	TTT			AGG		GAC	AGT	ATG	885
TTG (	GGG	GAT	CCC	AAG	AAG	CTG	CTC	ACC	CAA	CAT	TTC	GTG	CAG	927
GAA A	AAC	TAC	CTG	GAG	TAC	CGG	CAG	GTC	CCC	GGC	AGT	GAT	CCT	969
GCA :	TGT	TAT	GAA	TTC	CTG	TGG	GGT	CCA	AGG	GCC	CTC	GTT	GAA	1011
ACC A		TAT		AAA					ATG					1053
GGA (	GGA	CCT	CAC	TTA	TCC	TAC	CCA	CCC	CTG	CAT	GAG	TGG	GTT	1095
TTG Z	AGA	GAG	GGG	GAA	GAG	TGA								1116
GTCT														1166
GCAC	CTTC													1216
GGCC	CATI	CT I	rcac:	CTTI	rg az	AGCGA	AGCAC	F TC	AGCA?	TCT	TAG	CAGT	3GG	1266
TTTC	TGTI	CT (	GTTGC	SATGA	AC TI	TGAC	SATTA	A TTC	CTTTC	TTT	CCT	STTG	GAG	1316
TTGT'														1366
GTTT														1416
TAAG														1466
TTGT														1516
GAAT'	TAGO	CAA I	raac <i>i</i>	ATACA	AT GA	AGATA	AACTO	CAAC	CAAAE	CAA	AAG	ATAG:	ГTG	1566
ATTC			rgta(				CTG	L AA	ATTA	AAAC	AAA	CATG	CAA	1616
ACCA	GGAI	TT (	CCTT	BACTI	C T	TTG								1640.

- (2) INFORMATION FOR SEQUENCE ID NO: 12:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 943 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: single

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-31 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GGATCCTCCA	CCCCAGTAGA	GTGGGGACCT	CACAGAGTCT	GGCCAACCCT	50
CCTGACAGTT	CTGGGAATCC	GTGGCTGCGT	TTGCTGTCTG	CACATTGGGG	100
GCCCGTGGAT	TCCTCTCCCA	GGAATCAGGA	GCTCCAGGAA	CAAGGCAGTG	150
AGGACTTGGT	CTGAGGCAGT	GTCCTCAGGT	CACAGAGTAG	AGGGGGCTCA	200
<b>GATAG</b> TGCCA	ACGGTGAAGG	TTTGCCTTGG	ATTCAAACCA	AGGGCCCCAC	250
CTGCCCCAGA	ACACATGGAC	TCCAGAGCGC	CTGGCCTCAC	CCTCAATACT	300
TTCAGTCCTG	CAGCCTCAGC	ATGCGCTGGC	CGGATGTACC	CTGAGGTGCC	350
CTCTCACTTC	CTCCTTCAGG	TTCTGAGGGG	ACAGGCTGAC	CTGGAGGACC	400

AGAGGCCCCC GGAGGAGCAC TGAAGGAGAA GATCTGTAAG TAA	AGCCTTTG 450
TTAGAGCCTC CAAGGTTCCA TTCAGTACTC AGCTGAGGTC TCT	CACATGC 500
TCCCTCTCTC CCCAGGCCAG TGGGTCTCCA TTGCCCAGCT CCT	GCCCACA 550
CTCCCGCCTG TTGCCCTGAC CAGAGTCATC	580
ATG CCT CTT GAG CAG AGG AGT CAG CAC TGC AAG CCT	GAA GAA 622
GGC CTT GAG GCC CGA GGA GAG GCC CTG GGC CTG GTG	G GGT GCG 664
CAG GCT CCT GCT ACT GAG GAG CAG GAG GCT GCC TCC	TCC TCT 706
TCT AGT GTA GTT GAA GTC ACC CTG GGG GAG GTG CCT	GCT GCC 748
GAG TCA CCA GAT CCT CCC CAG AGT CCT CAG GGA GCC	TCC AGC 790
CTC CCC ACT ACC ATG AAC TAC CCT CTC TGG AGC CAA	A TCC TAT 832
GAG GAC TCC AGC AAC CAA GAA GAG GAG GGG CCA AGC	C ACC TTC 874
CCT GAC CTG GAG TCT GAG TTC CAA GCA GCA CTC AGT	AGG AAG 916
GTG GCC AAG TTG GTT CAT TTT CTG CTC	943

- (2) INFORMATION FOR SEQUENCE ID NO: 13:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2531 base pairs
      (B) TYPE: nucleic acid
      (C) STRANDEDNESS: single

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-4 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

GGATCCAGGC CCTGCCTGGA GAAATGTGAG GGCCCTGAGT GAACACAGTG	50
GGGATCATCC ACTCCATGAG AGTGGGGACC TCACAGAGTC CAGCCTACCC	100
TCTTGATGGC ACTGAGGGAC CGGGGCTGTG CTTACAGTCT GCACCCTAAG	150
GGCCCATGGA TTCCTCTCT AGGAGCTCCA GGAACAAGGC AGTGAGGCCT	200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCAGAGGATG CACAGGCTGT	250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACCAAGGGCC CCACCTGCCA	300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTCACCTCCC TACCATCAAT	350
CCTGCAGAAT CGACCTCTGC TGGCCGGCTA TACCCTGAGG TGCTCTCTCA	400
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAACCGGAGA CAGGATTCCC	450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATCTGTAAGT AAGCCTTTGT	500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGTCTCTCAC ATGCTCCCTC	550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGCTTTTGCC TGCACTCTTG	600
CCTGCTGCCC TGACCAGAGT CATC	624
ATG TCT TCT GAG CAG AAG AGT CAG CAC TGC AAG CCT GAG GAA	666
GGC GTT GAG GCC CAA GAA GAG GCC CTG GGC CTG GTG GGT GCA	708
CAG GCT CCT ACT ACT GAG GAG CAG GAG GCT GCT GTC TCC	750
TCC TCT CCT CTG GTC CCT GGC ACC CTG GAG GAA GTG CCT GCT	792
GCT GAG TCA GCA GGT CCT CCC CAG AGT CCT CAG GGA GCC TCT	834
GCC TTA CCC ACT ACC ATC AGC TTC ACT TGC TGG AGG CAA CCC	876
AAT GAG GGT TCC AGC AGC CAA GAA GAG GAG GGG CCA AGC ACC	918
TCG CCT GAC GCA GAG TCC TTG TTC CGA GAA GCA CTC AGT AAC	960
AAG GTG GAT GAG TTG GCT CAT TTT CTG CTC CGC AAG TAT CGA	1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATG CTG GAG AGA GTC	1044

ATC AAA AAT T	AC AAG CGC	TGC TTT	CCT GTG ATC	TTC GGC AAA	1086
GCC TCC GAG T	CC CTG AAG	ATG ATC	TTT GGC ATT	GAC GTG AAG	1128
GAA GTG GAC C			TAC ACC CTT		1170
•-• • • • • • •		GGC CTG	CTG GGT AAT	AAT CAG ATC	1212
TTT CCC AAG A	CA GGC CTI	CTG ATA	ATC GTC CTG	GGC ACA ATT	1254
GCA ATG GAG G	GC GAC AGC	GCC TCT	GAG GAG GAA	ATC TGG GAG	1296
	TG ATG GGG				1338
GTC TAT GGG G	AG CCC AGG	AAA CTG	CTC ACC CAA	GAT TGG GTG	1380
CAG GAA AAC T	AC CTG GAG	TAC CGG	CAG GTA CCC	GGC AGT AAT	1422
CCT GCG CGC T	AT GAG TTC	CTG TGG	GGT CCA AGG	GCT CTG GCT	1464
GAA ACC AGC T	AT GTG AAA	GTC CTG	GAG CAT GTG	GTC AGG GTC	1506
AAT GCA AGA G'	TT CGC ATI	GCC TAC	CCA TCC CTG	CGT GAA GCA	1548
GCT TTG TTA G	AG GAG GAA	GAG GGA	GTC TGA		1578
GCATGAGTTG CA	GCCAGGGC I	'GTGGGGAAG	GGGCAGGGCT	GGGCCAGTGC	1628
ATCTAACAGC CC'	TGTGCAGC A	GCTTCCCTI.	GCCTCGTGTA	ACATGAGGCC	1678
CATTCTTCAC TC'	TGTTTGAA G	AAAATAGTO	AGTGTTCTTA	GTAGTGGGTT	1728
TCTATTTTGT TG	GATGACTT G	GAGATTTAT	CTCTGTTTCC	TTTTACAATT	1778
GTTGAAATGT TC	CTTTTAAT G	GATGGTTGA	ATTAACTTCA	GCATCCAAGT	1828
TTATGAATCG TAG	GTTAACGT A	TATTGCTGT	TAATATAGTT	TAGGAGTAAG	1878
AGTCTTGTTT TT	TATTCAGA T	TGGGAAATC	CGTTCTATTT	TGTGAATTTG	1928
GGACATAATA AC	AGCAGTGG A	GTAAGTATT	TAGAAGTGTG	AATTCACCGT	1978
GAAATAGGTG AG	ATAAATTA A	AAGATACTT	AATTCCCGCC	TTATGCCTCA	2028
GTCTATTCTG TAX	AAATTTAA A	TATATAA	GCATACCTGG	ATTTCCTTGG	2078
CTTCGTGAAT GT	AAGAGAAA T	TAAATCTGA	TTAATAATA	CTTTCTGTTA	2128
ACTGGCTCAT TT	CTTCTCTA T	GCACTGAGC	: ATCTGCTCTG	TGGAAGGCCC	2178
AGGATTAGTA GT	GGAGATAC T	'AGGGTAAGC	CAGACACACA	CCTACCGATA	2228
GGGTATTAAG AG	TCTAGGAG C	GCGGTCATA	TAATTAAGGT	GACAAGATGT	2278
CCTCTAAGAT GT	AGGGGAAA A	GTAACGAGT	GTGGGTATGG	GGCTCCAGGT	2328
GAGAGTGGTC GG	GTGTAAAT T	CCCTGTGTG	GGGCCTTTTG	GGCTTTGGGA	2378
AACTGCATTT TC'	TTCTGAGG G	ATCTGATTC	TAATGAAGCT	TGGTGGGTCC	2428
AGGCCAGAT TC'	TCAGAGGG A	GAGGGAAAA	GCCCAGATTG	GAAAAGTTGC	2478
TCTGAGCAGT TC	CTTTGTGA C	AATGGATGA	ACAGAGAGGA	GCCTCTACCT	2528
GGG					2531

- (2) INFORMATION FOR SEQUENCE ID NO: 14:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2531 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS:single
  - (D) TOPOLOGY: linear
    (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-41 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

GGATCCAGGC	CCTGCCTGGA	GAAATGTGAG	GGCCCTGAGT	GAACACAGTG	50
GGGATCATCC	ACTCCATGAG	AGTGGGGACC	TCACAGAGTC	CAGCCTACCC	100
TCTTGATGGC	ACTGAGGGAC	CGGGGCTGTG	CTTACAGTCT	GCACCCTAAG	150

GGCCCATGGA TTCCTCTCT AGGAGCTCCA GGA TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCA GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACC	ACAAGGC AGTGAGGCCT 200
TGGTCTGAGA CAGTGTCCTC AGGTTACAGA GCA	GAGGATG CACAGGCTGT 250
GCCAGCAGTG AATGTTTGCC CTGAATGCAC ACC	CAAGGGCC CCACCTGCCA 300
CAAGACACAT AGGACTCCAA AGAGTCTGGC CTC	CACCTCCC TACCATCAAT 350
$-$ CCTCC $\lambda$ C $\lambda$ CTCTCTCCCCCCCCCCC $\lambda$ CT $\lambda$ CT	CCTCTCTCTCTCTCTCTCT
CTTCCTCCTT CAGGTTCTGA GCAGACAGGC CAA TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATC TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGT	ACCGGAGA CAGGATTCCC 450
TGGAGGCCAC AGAGGAGCAC CAAGGAGAAG ATC	TGTAAGT AAGCCTTTGT 500
TAGAGCCTCT AAGATTTGGT TCTCAGCTGA GGT	CTCTCAC ATGCTCCCTC 550
TCTCCGTAGG CCTGTGGGTC CCCATTGCCC AGC	TITITGCC TGCACTCTTG 600
CCTGCTGCCC TGAGCAGAGT CATC  ATG TCT TCT GAG CAG AAG AGT CAG CAC  GGC GTT GAG GCC CAA GAA GAG GCC CTG  CAG GCT CCT ACT ACT GAG GAG CAG GAG  TCC TCT CCT CTG GTC CCT GGC ACC CTG  GCT GAG TCA GCA GGT CCT CCC CAG AGT  GCC TTA CCC ACT ACC ATC AGC TTC ACT  AAT GAG GGT TCC AGC AGC CAA GAA GAG  TCG CCT GAC GCA GAG TCC TTG TTC CGA  AAG GTG GAT GAG TTG GCT CAT TTT CTG  GCC AAG GAG CTG GTC ACA AAG GCA GAA	624
ATG TCT TCT GAG CAG AAG AGT CAG CAC	TGC AAG CCT GAG GAA 666
GGC GTT GAG GCC CAA GAA GAG GCC CTG	GGC CTG GTG GGT GCG 708
CAG GCT CCT ACT ACT GAG GAG CAG GAG	GCT GCT GTC TCC TCC 750
TCC TCT CCT CTG GTC CCT GGC ACC CTG	GAG GAA GTG CCT GCT 792
GCT GAG TCA GCA GGT CCT CCC CAG AGT	CCT CAG GGA GCC TCT 834
GCC TTA CCC ACT ACC ATC AGC TTC ACT	TGC TGG AGG CAA CCC 876
AAT GAG GGT TCC AGC AGC CAA GAA GAG	GAG GGG CCA AGC ACC 918
TCG CCT GAC GCA GAG TCC TTG TTC CGA	GAA GCA CTC AGT AAC 960
AAG GTG GAT GAG TTG GCT CAT TTT CTG	CTC CGC AAG TAT CGA 1002
GCC AAG GAG CTG GTC ACA AAG GCA GAA ATC AAA AAT TAC AAG CGC TGC TTT CCT	ATG CTG GAG AGA GTC 1044
ATC AAA AAT TAC AAG CGC TGC TTT CCT	GTG ATC TTC GGC AAA 1086
GCC TCC GAG TCC CTG AAG ATG ATC TTT	GGC ATT GAC GTG AAG 1128
GAA GTG GAC CCC ACC AGC AAC ACC TAC	ACC CTT GTC ACC TGC 1170
ריים מכר רייד יירר ייאי מאיי מכר ריים ריים	$CCT$ $\Delta\Delta T$ $\Delta\Delta T$ $C\Delta C$ $\Delta TC$ 1212
TTT CCC AAG ACA GGC CTT CTG ATA ATC	GTC CTG GGC ACA ATT 1254
TTT CCC AAG ACA GGC CTT CTG ATA ATC GCA ATG GAG GGC GAC AGC GCC TCT GAG	GAG GAA ATC TGG GAG 1296
GAG CTG GGT GTG ATG GGG GTG TAT GAT	GGG AGG GAG CAC ACT 1338
GCA ATG GAG GGC GAC AGC GCC TCT GAG GAG CTG GGT GTG ATG GGG GTG TAT GAT GTC TAT GGG GAG CCC AGG AAA CTG CTC CAG GAA AAC TAC CTG GAG TAC CGG CAG CCT GCG CGC TAT GAG TTC CTG TGG GGT GAA ACC AGC TAT GTG AAA GTC CTG GAG AAT GCA AGA GTT CGC ATT GCC TAC CCA GCT TTG TTA GAG GAG GAA GAG GGA GTC	ACC CAA GAT TGG GTG 1380
CAG GAA AAC TAC CTG GAG TAC CGG CAG	GTA CCC GGC AGT AAT 1422
CCT GCG CGC TAT GAG TTC CTG TGG GGT	CCA AGG GCT CTG GCT 1464
GAA ACC AGC TAT GTG AAA GTC CTG GAG	CAT GTG GTC AGG GTC 1506
AAT GCA AGA GTT CGC ATT GCC TAC CCA	TCC CTG CGT GAA GCA 1548
GCT TTG TTA GAG GAG GAA GAG GGA GTC	TGA 1578
GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGG	SCAGGGCT GGGCCAGTGC 1628
GCT TTG TTA GAG GAG GAA GAG GGA GTC GCATGAGTTG CAGCCAGGGC TGTGGGGAAG GGC ATCTAACAGC CCTGTGCAGC AGCTTCCCTT GCC CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGT TCTATTTTGT TGGATGACTT GGAGATTTAT CTC	TCGTGTA ACATGAGGCC 1678
CATTCTTCAC TCTGTTTGAA GAAAATAGTC AGT	GTTCTTA GTAGTGGGTT 1728
TCTATTTTGT TGGATGACTT GGAGATTTAT CTC	TGTTTCC TTTTACAATT 1778
GIIGAAAIGI ICCIIIIAAI GGAIGGIIGA AII	AACTICA GCATCCAAGT 1020
TTATGAATCG TAGTTAACGT ATATTGCTGT TAA	
AGTCTTGTTT TTTATTCAGA TTGGGAAATC CGT	
GGACATAATA ACAGCAGTGG AGTAAGTATT TAG	
GAAATAGGTG AGATAAATTA AAAGATACTT AAT	
GTCTATTCTG TAAAATTTAA AAATATATAT GCA	
CTTCGTGAAT GTAAGAGAAA TTAAATCTGA ATA	
ACTGGCTCAT TTCTTCTCTA TGCACTGAGC ATC	
AGGATTAGTA GTGGAGATAC TAGGGTAAGC CAG	
GGGTATTAAG AGTCTAGGAG CGCGGTCATA TAA	
CCTCTAAGAT GTAGGGGAAA AGTAACGAGT GTG	
GAGAGTGGTC GGGTGTAAAT TCCCTGTGTG GGG	
AACTCCATTT TCTTCTGAGG GATCTGATTC TAA	
AGGGCCAGAT TCTCAGAGGG AGAGGGAAAA GCC	
TCTGAGCGGT TCCTTTGTGA CAATGGATGA ACA	GAGAGGA GCCTCTACCT 2528

GGG 2531

576670.1

- (2) INFORMATION FOR SEQUENCE ID NO: 15:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1068 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA to mRNA
  - (ix) FEATURE:
    - (A) NAME/KEY: cDNA MAGE-4
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

G	GGG	CCA	AGC	ACC	TCG	CCT	GAC	GCA	GAG	TCC	TTG	TTC	CGA	40
GAA	GCA	CTC	AGT	AAC	AAG	GTG	GAT	GAG	TTG	GCT	CAT	TTT	CTG	82
CTC	CGC	AAG	TAT	CGA	GCC	AAG	GAG	CTG	GTC	ACA	AAG	GCA	GAA	124
ATG	CTG	GAG	AGA	GTC	ATC	AAA	AAT	TAC	AAG	CGC	TGC	TTT	CCT	166
GTG	ATC	TTC	GGC	AAA	GCC	TCC	GAG	TCC	CTG	AAG	ATG	ATC	TTT	208
GGC	ATT	GAC	GTG	AAG	GAA	GTG	GAC	CCC	GCC	AGC	AAC	ACC	TAC	250
ACC	CTT	GTC	ACC	TGC	CTG	GGC	CTT	TCC	TAT	GAT	GGC	CTG	CTG	292
GGT	AAT	AAT	CAG	ATC	TTT	CCC	AAG	ACA	GGC	CTT	CTG	ATA	ATC	334
GTC	CTG	GGC	ACA	ATT	GCA	ATG	GAG	GGC	GAC	AGC	GCC	TCT	GAG	376
GAG	GAA	ATC	TGG	GAG	GAG	CTG	GGT	GTG	ATG	GGG	GTG	TAT	GAT	418
GGG	AGG	GAG	CAC	ACT	GTC	TAT	GGG	GAG	CCC	AGG	AAA	CTG	CTC	460
ACC	CAA	GAT	TGG	GTG	CAG	GAA	AAC	TAC	CTG	GAG	TAC	CGG	CAG	502
GTA	CCC	GGC	AGT	AAT	CCT	GCG	CGC	TAT	GAG	TTC	CTG	TGG	GGT	544
CCA	AGG	GCT	CTG	GCT	GAA	ACC	AGC	TAT	GTG	AAA	GTC	CTG	GAG	586
CAT	GTG	GTC	AGG	GTC	AAT	GCA	AGA	GTT	CGC	ATT	GCC	TAC	CCA	628
TCC	CTG	CGT	GAA	GCA	GCT	TTG	TTA	GAG	GAG	GAA	GAG	GGA	GTC	670
TGA	CATO	GAG :	rtgc <i>i</i>	AGCC	AG GO	GCTGT	rgggc	AA E	GGGG	CAGG	GCT	GGC	CAG	720
TGC	ATCT	AAC A	AGCCC	CTGTC	GC AC	GCAG(	CTTCC	CT	rgcc:	rcgt	GTA	ACATO	BAG	770
GCC	CATTO	CTT (	CACT	CTGTT	TT GA	AAGAA	AAATA	A GTO	CAGTO	FTTC	TTAC	GTAGT	rgg	820
GTTT	CTAI	TTT	rgttc	GATO	GA CI	rtgg <i>i</i>	\GAT'	CAT	rctc1	rgtt	TCCT	$\Gamma T T T T$	ACA	870
ATTO	STTGA	AAA :	rgttc	CCTTI	TT AA	ATGGA	ATGGT	TG	ATTA	AACT	TCAC	CAT	CCA	920
AGT	TAT	C AAE	CGT	AGTTA	AA CC	TAT?	ATTGO	TG	CAATT	ATA	GTTT	ragg <i>i</i>	AGT	970
AAG	AGTCT	rtg 1	CTTTT	TATT	C AC	SATTO	GGAA	ATC	CCGTT	CTA	TTTT	rgtg <i>f</i>	TA	1020
TTG	GACA	ATA A	AAT!	CAGC	AG TO	GAGI	[AAG]	TA	[TAG	AAGT	GTG	ATTC	7	1068

- (2) INFORMATION FOR SEQUENCE ID NO: 16:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2226 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-5 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT	CACCACACAC	50
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC		
		100
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT		150
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC		200
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA		250
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT		300
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC		350
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT	GAGGTGCCCT	400
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA	GGATCACCAG	450
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC	AAAGGAGAAG	500
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT		550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC		600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT		644
ATG TOT OTT GAG CAG AAG AGT CAG CAC TGC AAG		
		686
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC		728
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG		770
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC		812
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA		854
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA	GTA AGA AGG	896
TGG CTG ACT TGA		908
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCTGGT	CACAAAGGCA	958
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT	TTCCTGAGAT	1008
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC		1058
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC		1108
CTCCTATGAT GGCCTGCTGG TTGATAATAA TCAGATCATG		1158
GCCTCCTGAT AATCGTCTTG GGCATGATTG CAATGGAGGG		1208
CCTGAGGAGA AAATCTGGGA GGAGCTGAGT GTGATGAAGG		1258
GAGGGAGCAC AGTGTCTGTG GGGAGCCCAG GAAGCTGCTC		1308
TGGTGCAGGA AAACTACCTG GAGTACCGGC AGGTGCCCAG		1358
ATATGCTATG AGTTACTGTG GGGTCCAAGG GCACTCGCTG		1408
CTGGAGCACG TGGTCAGGGT CAATGCAAGA GTTCTCATTT		1458
CCTGCGTGAA GCAGCTTTGA GAGAGGAGGA AGAGGGAGTC	TGAGCATGAG	1508
CTGCAGCCAG GGCCACTGCG AGGGGGGCTG GGCCAGTGCA	CCTTCCAGGG :	1558
CTCCGTCCAG TAGTTTCCCC TGCCTTAATG TGACATGAGG	CCCATTCTTC	1608
TCTCTTTGAA GAGAGCAGTC AACATTCTTA GTAGTGGGTT	TCTGTTCTAT	1658
TGGATGACTT TGAGATTTGT CTTTGTTTCC TTTTGGAATT	GTTCAAATGT	1708
TTCTTTTAAT GGGTGGTTGA ATGAACTTCA GCATTCAAAT	TTATGAATGA	1758
CAGTAGTCAC ACATAGTGCT GTTTATATAG TTTAGGAGTA		1808
TTTTTATTCA GATTGGGAAA TCCATTCCAT TTTGTGAATT		1858
TACAGCAGTG GAATAAGTAT TCATTTAGAA ATGTGAATGA		1908
TGATGACATA AAGAAATTAA AAGATATTTA ATTCTTGCTT		1958
		2008
TATTCGGTAA AATTTTTTT AAAAAATGTG CATACCTGGA		
TTCTTTGAGA ATGTAAGACA AATTAAATCT GAATAAATCA		2058
TCACTGGCTC ATTTATTCTC TATGCACTGA GCATTTGCTC		2108
CCTGGGTTAA TAGTGGAGAT GCTAAGGTAA GCCAGACTCA		2158
CAGGGTAGTA AAGTCTAGGA GCAGCAGTCA TATAATTAAG		2208
GCCCTCTAAG ATGTAGAG	:	2226

- (2) INFORMATION FOR SEQUENCE ID NO: 17:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2305 base pairs
    - (B) TYPE; nucleic acid(C) STRANDEDNESS: single

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-51 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

	G1 GG1 G1 G1 G
GGATCCAGGC CTTGCCAGGA GAAAGGTGAG GGCCCTGTGT	
GGGACCATTC ACCCCAAGAG GGTGGAGACC TCACAGATTC	
TCCTGTTAGC ACTGGGGGCC TGAGGCTGTG CTTGCAGTCT	
GGCCCATGCA TTCCTCTTCC AGGAGCTCCA GGAAACAGAC	
TGGTCTGAGG CCGTGCCCTC AGGTCACAGA GCAGAGGAGA	
TAGTGCCAGC AGTGAACGTT TGCCTTGAAT GCACACTAAT	
GCCCCAGAAC ATATGGGACT CCAGAGCACC TGGCCTCACC	
TCAGTCCTGC AGAATCAGCC TCTGCTTGCT TGTGTACCCT	
CTCACTTTTT CCTTCAGGTT CTCAGGGGAC AGGCTGACCA	
GAAGCTCCAG AGGATCCCCA GGAGGCCCTA GAGGAGCACC	
ATCTGTAAGT AAGCCTTTGT TAGAGCCTCC AAGGTTCAGT	TTTTAGCTGA 550
GGCTTCTCAC ATGCTCCCTC TCTCTCCAGG CCAGTGGGTC	TCCATTGCCC 600
AGCTCCTGCC CACACTCCTG CCTGTTGCGG TGACCAGAGT	CGTC 644
ATG TCT CTT GAG CAG AAG AGT CAG CAC TGC AAG	CCT GAG GAA 686
GGC CTT GAC ACC CAA GAA GAG CCC TGG GCC TGG	TGG GTG TGC 728
AGG CTG CCA CTA CTG AGG AGC AGG AGG CTG TGT	CCT CCT CCT 770
CTC CTC TGG TCC CAG GCA CCC TGG GGG AGG TGC	CTG CTG CTG 812
GGT CAC CAG GTC CTC TCA AGA GTC CTC AGG GAG	CCT CCG CCA 854
TCC CCA CTG CCA TCG ATT TCA CTC TAT GGA GGC	AAT CCA TTA 896
AGG GCT CCA GCA ACC AAG AAG AGG AGG GGC CAA	GCA CCT CCC 938
CTG ACC CAG AGT CTG TGT TCC GAG CAG CAC TCA	GTA AGA AGG 980
TGG CTG ACT TGA	992
TTCATTTTCT GCTCCTCAAG TATTAAGTCA AGGAGCCGGT	CACAAAGGCA 1042
GAAATGCTGG AGAGCGTCAT CAAAAATTAC AAGCGCTGCT	TTCCTGAGAT 1092
CTTCGGCAAA GCCTCCGAGT CCTTGCAGCT GGTCTTTGGC	ATTGACGTGA 1142
AGGAAGCGGA CCCCACCAGC AACACCTACA CCCTTGTCAC	CTGCCTGGGA 1192
CTCCTATGAT GGCCTGGTGG TTTAATCAGA TCATGCCCAA	GACGGGCCTC 1242
CTGATAATCG TCTTGGGCAT GATTGCAATG GAGGGCAAAT	GCGTCCCTGA 1292
GGAGAAAATC TGGGAGGAGC TGGGTGTGAT GAAGGTGTAT	GTTGGGAGGG 1342
AGCACAGTGT CTGTGGGGAG CCCAGGAAGC TGCTCACCCA	
CAGGAAAACT ACCTGGAGTA CCGCAGGTGC CCAGCAGTGA	
TATGAGTTAC TGTGGGGTCC AAGGGCACTC GCTGCTTGAA	
CACGTGGTCA GGGTCAATGC AAGAGTTCTC ATTTCCTACC	
TGAAGCAGCT TTGAGAGAGG AGGAAGAGGG AGTCTGAGCA	
CCAGGGCCAC TGCGAGGGGG GCTGGGCCAG TGCACCTTCC	
CCAGTAGTTT CCCCTGCCTT AATGTGACAT GAGGCCCATT	
TGAAGAGAC AGTCAACATT CTTAGTAGTG GGTTTCTGTT	
ACTTTGAGAT TTGTCTTTGT TTCCTTTTGG AATTGTTCAA	
TAATGGGTGG TTGAATGAAC TTCAGCATTC AAATTTATGA	
ILLICOTO TIGHTONIO TIGHOMITO INNITITION	

TCACACATAG	TGCTGTTTAT	ATAGTTTAGG	AGTAAGAGTC	TTGTTTTTTA	1892
TTCAGATTGG	GAAATCCATT	CCATTTTGTG	AATTGGGACA	TAGTTACAGC	1942
<b>A</b> GTGGAATAA	GTATTCATTT	AGAAATGTGA	ATGAGCAGTA	AAACTGATGA	1992
GATAAAGAAA	TTAAAAGATA	TTTAATTCTT	GCCTTATACT	CAGTCTATTC	2042
GGTAAAATTT	TTTTTTAAAA	ATGTGCATAC	CTGGATTTCC	TTGGCTTCTT	2092
TGAGAATGTA	AGACAAATTA	AATCTGAATA	AATCATTCTC	CCTGTTCACT	2142
GGCTCATTTA	TTCTCTATGC	ACTGAGCATT	TGCTCTGTGG	AAGGCCCTGG	2192
GTTAATAGTG	GAGATGCTAA	GGTAAGCCAG	ACTCACCCCT	ACCCACAGGG	2242
TAGTAAAGTC	TAGGAGCAGC	AGTCATATAA	TTAAGGTGGA	GAGATGCCCT	2292
CTAAGATGTA	GAG				2305

- (2) INFORMATION FOR SEQUENCE ID NO: 18:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 225 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: cDNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-6 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TAT	TTC	TTT	CCT	GTG	ATC	TTC	AGC	AAA	GCT	TCC	GAT	TCC	TTG	42
CAG	CTG	GTC	TTT	GGC	ATC	GAG	CTG	ATG	GAA	GTG	GAC	CCC	ATC	84
GGC	CAC	GTG	TAC	ATC	TTT	GCC	ACC	TGC	CTG	GGC	CTC	TCC	TAC	126
GAT	GGC	CTG	CTG	GGT	GAC	AAT	CAG	ATC	ATG	CCC	AGG	ACA	GGC	168
TTC	CTG	ATA	ATC	ATC	CTG	GCC	ATA	ATC	GCA	AGA	GAG	GGC	GAC	210
TGT	GCC	CCT	GAG	GAG										225

- (2) INFORMATION FOR SEQUENCE ID NO: 19:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1947 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-7 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGAATGGACA	ACAAGGGCCC	CACACTCCCC	AGAACACAAG	GGACTCCAGA	50
GAGCCCAGCC	TCACCTTCCC	TACTGTCAGT	CCTGCAGCCT	CAGCCTCTGC	100
TGGCCGGCTG	TACCCTGAGG	TGCCCTCTCA	CTTCCTCCTT	CAGGTTCTCA	150
GCGGACAGGC	CGGCCAGGAG	GTCAGAAGCC	CCAGGAGGCC	CCAGAGGAGC	200

ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC	TCCAGGGCGT	250
GGTTCACAAA TGAGGCCCCT CACAAGCTCC TTCTCTCCCC	AGATCTGTGG	300
GTTCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT	GCTGCCCTGA	350
CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG		400
GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT	GGGTGCGCAG	450
GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA	CTCTGATTGA	500
AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT	CCTCCCTGA	550
GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC	ACTCTATGGA	600
GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG	GCCAACCACC	650
TAGACACACC CCGCTCACCT GGCGTCCTTG TTCCA		685
ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC	TGC ACA AGT	727
ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA	TGC TGG ACA	769
GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT	GTG ATC TAT	811
GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT	GGC ATT GAC	853
ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG	TCC TTG TCA	895
CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG	GTG ATG ATC	937
AGA GCA TGC CCG AGA CCG GCC TTC TGA		964
TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC		1014
GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA	TGGAGCAGTT	1064
TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT	GCAGGAAAAC	1114
TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT	GCTACCAGTT	1164
CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG	AAAGTCCTGG	1214
AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA	CCCATCCCTG	1264
CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG	CAGAAGTTGC	1314
AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA	GTGCACGTTC	1364
CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC	ATTCTTCACT	1414
CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG	AGTGTGTTGG	1464
GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT	TCTCTTGGGC	1514
GATTTGGAGG TTTATCTTTG TTTCCTTTTG CAGTCGTTCA	AATGTTCCTT	1564
TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT	ATGACAGTAG	1614
GCAGACTTAC TGTTTTTTAT ATAGTTAAAA GTAAGTGCAT	TGTTTTTAT	1664
TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA	CATAACATAG	1714
CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC	GGTAAAATGG	1764
GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG	GTGGCTCACG	1814
CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT	CACGAGGTCA	1864
GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT	CTCTATTAAA	1914
AATACAAAC TTAGCCGGGC GTGGTGGCGG GTG		1947

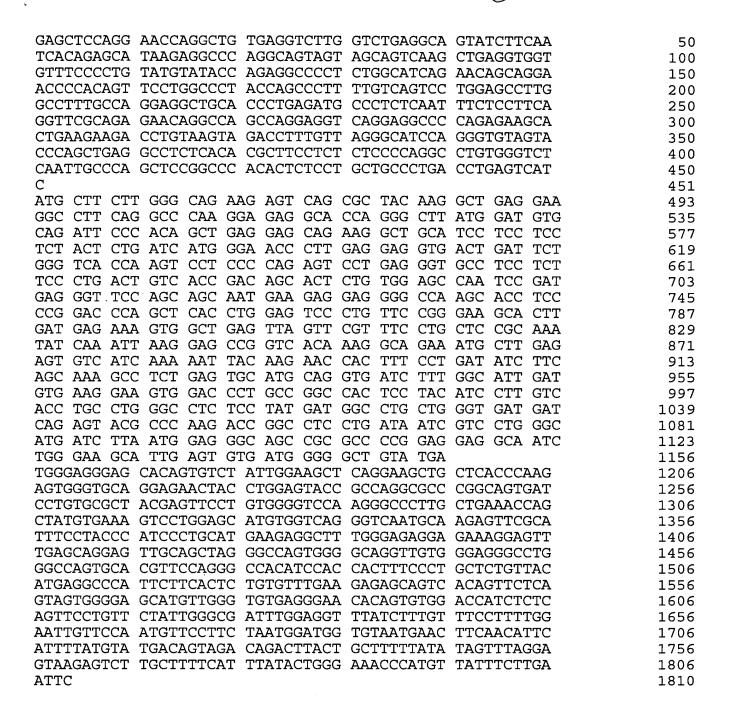
- (2) INFORMATION FOR SEQUENCE ID NO: 20:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1810 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: single

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-8 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ACCGAAGGAG AAGATCTGTA AGTAGGCCTT TGTTAGGGCC TCCAGGGCGT	250
GGTTCACAAA TGAGGCCCCT CACAAGCTCC TTCTCTCCCC AGATCTGTGG	300
GTTCCTCCCC ATCGCCCAGC TGCTGCCCGC ACTCCAGCCT GCTGCCCTGA	350
CCAGAGTCAT CATGTCTTCT GAGCAGAGGA GTCAGCACTG CAAGCCTGAG	400
GATGCCTTGA GGCCCAAGGA CAGGAGGCTC TGGGCCTGGT GGGTGCGCAG	450
GCTCCCGCCA CCGAGGAGCA CGAGGCTGCC TCCTCCTTCA CTCTGATTGA	500
AGGCACCCTG GAGGAGGTGC CTGCTGCTGG GTCCCCCAGT CCTCCCCTGA	550
GTCTCAGGGT TCCTCCTTTT CCCTGACCAT CAGCAACAAC ACTCTATGGA	600
GCCAATCCAG TGAGGGCACC AGCAGCCGGG AAGAGGAGGG GCCAACCACC	650
TAGACACAC CCGCTCACCT GGCGTCCTTG TTCCA	685
ATG GGA AGG TGG CTG AGT TGG TTC GCT TCC TGC TGC ACA AGT	727
ATC GAG TCA AGG AGC TGG TCA CAA AGG CAG AAA TGC TGG ACA	769
GTG TCA TCA AAA ATT ACA AGC ACT AGT TTC CTT GTG ATC TAT	811
GGC AAA GCC TCA GAG TGC ATG CAG GTG ATG TTT GGC ATT GAC	853
ATG AAG GAA GTG GAC CCC GCG GCC ACT CCT ACG TCC TTG TCA	895
CCT GCT TGG GCC TCT CCT ACA ATG GCC TGC TGG GTG ATG ATC	937
AGA GCA TGC CCG AGA CCG GCC TTC TGA	964
TTATGGTCTT GACCATGATC TTAATGGAGG GCCACTGTGC CCCTGAGGAG	1014
GCAATCTGGG AAGCGTTGAG TGTAATGGTG TATGATGGGA TGGAGCAGTT	1064
TCTTTGGGCA GCTGAGGAAG CTGCTCACCC AAGATTGGGT GCAGGAAAAC	1114
TACCTGCAAT ACCGCCAGGT GCCCAGCAGT GATCCCCCGT GCTACCAGTT	1164
CCTGTGGGGT CCAAGGGCCC TCATTGAAAC CAGCTATGTG AAAGTCCTGG	1214
AGTATGCAGC CAGGGTCAGT ACTAAAGAGA GCATTTCCTA CCCATCCCTG	1264
CATGAAGAGG CTTTGGGAGA GGAGGAAGAG GGAGTCTGAG CAGAAGTTGC	1314
AGCCAGGGCC AGTGGGGCAG ATTGGGGGAG GGCCTGGGCA GTGCACGTTC	1364
CACACATCCA CCACCTTCCC TGTCCTGTTA CATGAGGCCC ATTCTTCACT	1414
CTGTGTTTGA AGAGAGCAGT CAATGTTCTC AGTAGCGGGG AGTGTGTTGG	1464
GTGTGAGGGA ATACAAGGTG GACCATCTCT CAGTTCCTGT TCTCTTGGGC	1514
GATTTGGAGG TTTATCTTTG TTTCCTTTTG CAGTCGTTCA AATGTTCCTT	1564
TTAATGGATG GTGTAATGAA CTTCAACATT CATTTCATGT ATGACAGTAG	1614
GCAGACTTAC TGTTTTTAT ATAGTTAAAA GTAAGTGCAT TGTTTTTAT	1664
TTATGTAAGA AAATCTATGT TATTTCTTGA ATTGGGACAA CATAACATAG	1714
CAGAGGATTA AGTACCTTTT ATAATGTGAA AGAACAAAGC GGTAAAATGG	1764
GTGAGATAAA GAAATAAAGA AATTAAATTG GCTGGGCACG GTGGCTCACG	1814
CCTGTAATCC CAGCACTTTA GGAGGCAGAG GCACGGGGAT CACGAGGTCA	1864
GGAGATCGAG ACCATTCTGG CTAACACAGT GAAACACCAT CTCTATTAAA	1914
AATACAAAAC TTAGCCGGGC GTGGTGGCGG GTG	1947

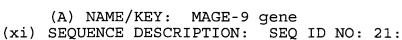
- (2) INFORMATION FOR SEQUENCE ID NO: 20:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1810 base pairs
    - (B) TYPE: nucleic acid(C) STRANDEDNESS: single

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-8 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:



## (2) INFORMATION FOR SEQUENCE ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 1412 base pairs
  - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: genomic DNA
- (ix) FEATURE:



TCTGAGACAG TGTCCTCAGG TCGCAGA	GCA GAGGAGACCC	AGGCAGTGTC	50
AGCAGTGAAG GTGAAGTGTT CACCCTG			100
GCCCCAGCAC ACATGGGACC CCATAGC			150
TCACTCATAG AGCCTTGATC TCTGCAG	GCT AGCTGCACGC	TGAGTAGCCC	200
TCTCACTTCC TCCCTCAGGT TCTCGGG			250
GCCCCAAGAG GCCCCAGAGC AGCACTG			300
TGTTAGAACC TCCAAGGTTC GGTTCTC	AGC TGAAGTCTCT	CACACACTCC	350
CTCTCTCCCC AGGCCTGTGG GTCTCCA			400
CTGACTGCTG CCCTGACCAG AGTCATC			427
ATG TCT CTC GAG CAG AGG AGT C	CG CAC TGC AAG	CCT GAT GAA	469
GAC CTT GAA GCC CAA GGA GAG G			511
CAG GAA CCC ACA GGC GAG GAG G	AG GAG ACT ACC	TCC TCC TCT	553
GAC AGC AAG GAG GAG GTG T	CT GCT GCT GGG	TCA TCA AGT	595
CCT CCC CAG AGT CCT CAG GGA G	GC GCT TCC TCC	TCC ATT TCC	637
		GGC TCC AGC	679
AGT CAA GAA GAG GAA GAG CCA A	GC TCC TCG GTC	GAC CCA GCT	721
CAG CTG GAG TTC ATG TTC CAA G	AA GCA CTG AAA	TTG AAG GTG	763
GCT GAG TTG GTT CAT TTC CTG C	TC CAC AAA TAT	CGA GTC AAG	805
GAG CCG GTC ACA AAG GCA GAA A	TG CTG GAG AGC	GTC ATC AAA	847
AAT TAC AAG CGC TAC TTT CCT G	TG ATC TTC GGC	AAA GCC TCC	889
GAG TTC ATG CAG GTG ATC TTT G			931
GAC CCC GCC GGC CAC TCC TAC A	TC CTT GTC ACT	GCT CTT GGC	973
CTC TCG TGC GAT AGC ATG CTG G	GT GAT GGT CAT	AGC ATG CCC	1015
AAG GCC GCC CTC CTG ATC ATT G	TC CTG GGT GTG	ATC CTA ACC	1057
AAA GAC AAC TGC GCC CCT GAA G	AG GTT ATC TGG	GAA GCG TTG	1099
AGT GTG ATG GGG GTG TAT GTT G	GG AAG GAG CAC	ATG TTC TAC	1141
GGG GAG CCC AGG AAG CTG CTC A	CC CAA GAT TGG	GTG CAG GAA	1183
AAC TAC CTG GAG TAC CGG CAG G	TG CCC GGC AGT	GAT CCT GCG	1225
CAC TAC GAG TTC CTG TGG GGT T			1267
AGC TAT GAG AAG GTC ATA AAT T	AT TTG GTC ATG	CTC AAT GCA	1309
AGA GAG CCC ATC TGC TAC CCA T	CC CTT TAT GAA	GAG GTT TTG	1351
GGA GAG GAG CAA GAG GGA GTC T			1375
GCACCAGCCG CAGCCGGGGC CAAAGTT	TGT GGGGTCA		1412

- (2) INFORMATION FOR SEQUENCE ID NO: 22:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 920 base pairs
    - (B) TYPE: nucleic acid
    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-10 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

ACCTGCTCCA GGACAAAGTG GACCCCACTG CATCAGCTCC	C ACCTACCCTA 50
CTGTCAGTCC TGGAGCCTTG GCCTCTGCCG GCTGCATCCT	T GAGGAGCCAT 100
CTCTCACTTC CTTCTTCAGG TTCTCAGGGG ACAGGGAGAG	G CAAGAGGTCA 150
AGAGCTGTGG GACACCACAG AGCAGCACTG AAGGAGAAGA	A CCTGTAAGTT 200
GGCCTTTGTT AGAACCTCCA GGGTGTGGTT CTCAGCTGTC	G GCCACTTACA 250
CCCTCCCTCT CTCCCCAGGC CTGTGGGTCC CCATCGCCCA	A AGTCCTGCCC 300
ACACTCCCAC CTGCTACCCT GATCAGAGTC ATC	333
ATG CCT CGA GCT CCA AAG CGT CAG CGC TGC ATC	G CCT GAA GAA 379
GAT CTT CAA TCC CAA AGT GAG ACA CAG GGC CTC	C GAG GGT GCA 41°
CAG GCT CCC CTG GCT GTG GAG GAG GAT GCT TCA	A TCA TCC ACT 459
TCC ACC AGC TCC TCT TTT CCA TCC TCT TTT CCC	C TCC TCC TCC 50:
TCT TCC TCC TCC TCC TGC TAT CCT CTA ATA	A CCA AGC ACC 543
CCA GAG GAG GTT TCT GCT GAT GAT GAG ACA CCA	A AAT CCT CCC 589
CAG AGT GCT CAG ATA GCC TGC TCC TCC CCC TCC	G GTC GTT GCT 62
TCC CTT CCA TTA GAT CAA TCT GAT GAG GGC TCC	C AGC AGC CAA 669
AAG GAG GAG AGT CCA AGC ACC CTA CAG GTC CTC	G CCA GAC AGT 71:
GAG TCT TTA CCC AGA AGT GAG ATA GAT GAA AAC	G GTG ACT GAT 753
TTG GTG CAG TTT CTG CTC TTC AAG TAT CAA ATC	G AAG GAG CCG 795
ATC ACA AAG GCA GAA ATA CTG GAG AGT GTC ATA	A AAA AAT TAT 83°
GAA GAC CAC TTC CCT TTG TTG TTT AGT GAA GCC	C TCC GAG TGC 879
ATG CTG CTG GTC TTT GGC ATT GAT GTA AAG GAA	A GTG GAT CC 920

- (2) INFORMATION FOR SEQUENCE ID NO: 23:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 1107 base pairs (B) TYPE: nucleic acid

    - (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: MAGE-11 gene
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

AGAGAACAGG CCAACCTGGA GGACAGGAGT CCCAGGAGAA CCCAGAGGAT	50
CACTGGAGGA GAACAAGTGT AAGTAGGCCT TTGTTAGATT CTCCATGGTT	100
CATATCTCAT CTGAGTCTGT TCTCACGCTC CCTCTCTCCC CAGGCTGTGG	150
GGCCCCATCA CCCAGATATT TCCCACAGTT CGGCCTGCTG ACCTAACCAG	200
AGTCATCATG CCTCTTGAGC AAAGAAGTCA GCACTGCAAG CCTGAGGAAG	250
CCTTCAGGCC CAAGAAGAAG ACCTGGGCCT GGTGGGTGCA CAGGCTCTCC	300
AAGCTGAGGA GCAGGAGGCT GCCTTCTTCT CCTCTACTCT GAATGTGGGC	350
ACTCTAGAGG AGTTGCCTGC TGCTGAGTCA CCAAGTCCTC CCCAGAGTCC	400
TCAGGAAGAG TCCTTCTCTC CCACTGCCAT GGATGCCATC TTTGGGAGCC	450
TATCTGATGA GGGCTCTGGC AGCCAAGAAA AGGAGGGGCC AAGTACCTCG	500
CCTGACCTGA TAGACCCTGA GTCCTTTTCC CAAGATATAC TACATGACAA	550
GATAATTGAT TTGGTTCATT TATTCTCCGC AAGTATCGAG TCAAGGGGCT	600
GATCACAAAG GCAGAA	616
ATG CTG GGG AGT GTC ATC AAA AAT TAT GAG GAC TAC TTT CCT	658
GAG ATA TTT AGG GAA GCC TCT GTA TGC ATG CAA CTG CTC TTT	700

GGC	ATT	GAT	GTG	AAG	GAA	GTG	GAC	CCC	ACT	AGC	CAC	TCC	TAT	742
GTC	CTT	GTC	ACC	TCC	CTC	AAC	CTC	TCT	TAT	GAT	GGC	ATA	CAG	784
TGT	AAT	GAG	CAG	AGC	ATG	CCC	AAG	TCT	GGC	CTC	CTG	ATA	ATA	826
GTC	CTG	GGT	GTA	ATC	TTC	ATG	GAG	GGG	AAC	TGC	ATC	CCT	GAA	868
GAG	GTT	ATG	TGG	GAA	GTC	CTG	AGC	ATT	ATG	GGG	GTG	TAT	GCT	910
GGA	AGG	GAG	CAC	TTC	CTC	TTT	GGG	GAG	CCC	AAG	AGG	CTC	CTT	952
ACC	CAA	AAT	TGG	GTG	CAG	GAA	AAG	TAC	CTG	GTG	TAC	CGG	CAG	994
GTG	CCC	GGC	ACT	GAT	CCT	GCA	TGC	TAT	GAG	TTC	CTG	TGG	GGT	1036
CCA	AGG	GCC	CAC	GCT	GAG	ACC	AGC	AAG	ATG	AAA	GTT	CTT	GAG	1078
TAC	ATA	GCC	AAT	GCC	AAT	GGG	AGG	GAT	CC					1107

- (2) INFORMATION FOR SEQUENCE ID NO: 24:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2150 base pairs
    - (B) TYPE: nucleic acid (C) STRANDEDNESS: single

    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA
  - (ix) FEATURE:
    - (A) NAME/KEY: smage-I
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TCTGTCTGCA TATGCCTCCA C	TTGTGTGTA GCAGTCTC	A ATGGATCTCT	50
CTCTACAGAC CTCTGTCTGT G			100
ACAGGTTTCT GCCCCTGCAT G			150
TATACCCCTG CATTGTAAGT T			200
GCCCTTGTAT GCAGGCCTAA G			250
AAGCTAGTGA AAGATCTAAC C			300
ATGCAGTGGC CTAACAAGTT T			350
AGCTTGATCC ACGAGTTCAG A			394
ATG TTC TCC TGG AAA GCT			436
CCA AGG TAT TCT CTA CCT	GGT AGT ACA GAG G	CA CTT ACA GGT	478
TGT CAT TCT TAT CCT TCC			520
ACT TCA GCC CTG AGC ACA	GTC AAC ATG CCT AC	G GGT CAA AAG	565
AGT AAG ACC CGC TCC CGT	GCA AAA CGA CAG CA	G TCA CGC AGG	604
GAG GTT CCA GTA GTT CAG	CCC ACT GCA GAG GA	A GCA GGG TCT	646
TCT CCT GTT GAC CAG AGT	GCT GGG TCC AGC T	C CCT GGT GGT	688
TCT GCT CCT CAG GGT GTG	AAA ACC CCT GGA TO	T TTT GGT GCA	730
GGT GTA TCC TGC ACA GGC	TCT GGT ATA GGT GC	T AGA AAT GCT	772
GCT GTC CTG CCT GAT ACA	AAA AGT TCA GAT GO	C ACC CAG GCA	814
GGG ACT TCC ATT CAG CAC	ACA CTG AAA GAT CO	T ATC ATG AGG	856
AAG GCT AGT GTG CTG ATA	GAA TTC CTG CTA GA	AT AAA TTT AAG	898
ATG AAA GAA GCA GTT ACA	AGG AGT GAA ATG CT	G GCA GTA GTT	940
AAC AAG AAG TAT AAG GAG	CAA TTC CCT GAG AT	C CTC AGG AGA	982
ACT TCT GCA CGC CTA GAA			1024
GAA ATT GAT CCC AGC ACT			1066
CTG GGT CTT TCC ACT GAG			1108
TTG CCT AGG ACA GGT CTC			1150
TTC ATG AAG GGT AAC CGT			1192
TTT CTG CAT GGA GTG GGG			1234
ATC TTT GGC GAG CCT GAG			1276
GAA AAT TAC CTG GAG TAC			1314
CCA AGC TAT GAG TTC CTG			1360
ACA ACC AAG ATG AAA GTO			1402
GGC ACA GTC CCT AGT GCC			1444
CTT AGA GAT CAG GCA GGA			1486
GGC AAG GGT GTT CAT TCC	AAG GCC CCA TCC CA	A AAG TCC TCT	1528
AAC ATG TAG			1537
TTGAGTCTGT TCTGTTGTGT T			1587
AGAGTTCATA GCCTACCAGA A			1637
ACATTAGTAG AATGGAGGCT A	TTTTTGTTA CTTTTCAA	AT GTTTGTTTAA	1687

CTAAACAGTG CTTTTTGCCA	TGCTTCTTGT	TAACTGCATA	AAGAGGTAAC	1737
TGTCACTTGT CAGATTAGGA	CTTGTTTTGT	TATTTGCAAC	AAACTGGAAA	1787
ACATTATTTT GTTTTTACTA	AAACATTGTG	TAACATTGCA	TTGGAGAAGG	1837
GATTGTCATG GCAATGTGAT	ATCATACAGT	GGTGAAACAA	CAGTGAAGTG	1887
GGAAAGTTTA TATTGTTAAT	TTTGAAAATT	TTATGAGTGT	GATTGCTGTA	1937
TACTTTTTC TTTTTTGTAT	AATGCTAAGT	GAAATAAAGT	TGGATTTGAT	1987
GACTTTACTC AAATTCATTA	GAAAGTAAAT	CGTAAAACTC	TATTACTTTA	2037
TTATTTTCTT CAATTATGAA	TTAAGCATTG	GTTATCTGGA	AGTTTCTCCA	2087
GTAGCACAGG ATCTAGTATG	AAATGTATCT	AGTATAGGCA	CTGACAGTGA	2137
GTTATCAGAG TCT				2150

- (2) INFORMATION FOR SEQUENCE ID NO: 25:
  - (i) SEQUENCE CHARACTERISTICS:
    - (A) LENGTH: 2099 base pairs (B) TYPE: nucleic acid

    - (B) TYPE: nucleic acid (C) STRANDEDNESS: single
    - (D) TOPOLOGY: linear
  - (ii) MOLECULE TYPE: genomic DNA

  - (ix) FEATURE:
    (A) NAME/KEY: smage-II
  - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCTTATTGG	GTCTGTCTGC	ATATGCCTCC	ACTTGTGTGT	AGCAGTCTCA	50
AATGGATCTC	TCTCTACAGA	CCTCTGTCTG	TGTCTGGCAC	CCTAAGTGGC	100
TTTGCATGGG	CACAGGTTTC	TGCCCCTGCA	TGGAGCTTAA	ATAGATCTTT	150
CTCCACAGGC	CTATACCCCT	GCATTGTAAG	TTTAAGTGGC	TTTATGTGGA	200
TACAGGTCTC	TGCCCTTGTA	TGCAGGCCTA	AGTTTTTCTG	TCTGCTTAGC	250
CCCTCCAAGT	GAAGCTAGTG	AAAGATCTAA	CCCACTTTTG	GAAGTCTGAA	300
ACTAGACTTT	TATGCAGTGG	CCTAACAAGT	TTTAATTTCT	TCCACAGGGT	350
TTGCAGAAAA	GAGCTTGATC	CACGAGTTCG	GAAGTCCTGG	TATGTTCCTA	400
GAAAGATGTT	CTCCTGGAAA	GCTTCAAAAG	CCAGGTCTCC	ATTAAGTCCA	450
AGGTATTCTC	TACCTGGTAG	TACAGAGGTA	CTTACAGGTT	GTCATTCTTA	500
TCTTTCCAGA	TTCCTGTCTG	CCAGCTCTTT	TACTTCAGCC	CTGAGCACAG	550
TCAACATGCC	TAGGGGTCAA	AAGAGTAAGA	CCCGCTCCCG	TGCAAAACGA	600
CAGCAGTCAC	GCAGGGAGGT	TCCAGTAGTT	CAGCCCACTG	CAGAGGAAGC	650
AGGGTCTTCT	CCTGTTGACC	AGAGTGCTGG	GTCCAGCTTC	CCTGGTGGTT	700
CTGCTCCTCA	GGGTGTGAAA	ACCCCTGGAT	CTTTTGGTGC	AGGTGTATCC	750
TGCACAGGCT	CTGGTATAGG	TGGTAGAAAT	GCTGCTGTCC	TGCCTGATAC	800
AAAAAGTTCA	GATGGCACCC	AGGCAGGGAC	TTCCATTCAG	CACACACTGA	850
AAGATCCTAT	CATGAGGAAG	GCTAGTGTGC	TGATAGAATT	CCTGCTAGAT	900
AAGTTTAAGA	TGAAAGAAGC	AGTTACAAGG	AGTGAAATGC	TGGCAGTAGT	950
TAACAAGAAG	TATAAGGAGC	AATTCCCTGA	GATCCTCAGG	AGAACTTCTG	1000
CACGCCTAGA		GGTCTTGAGT	TGAAGGAAAT	TGATCCCAGC	1050
ACTCATTCCT	ATTTGCTGGT	AGGCAAACTG	GGTCTTTCCA	CTGAGGGAAG	1100
TTTGAGTAGT	AACTGGGGGT	TGCCTAGGAC	AGGTCTCCTA		1150
TAGGTGTGAT	CTTCATGAAG	GGTAACCGTG	<b>4 41 1 4 1 1 1 1 1 1 1</b>	AGAGGTCTGG	1200
CAATTTCTGC	ATGGAGTGGG	GGTATATGCT	GGGAAGAAGC		1250
TGGCGAGCCT	GAGGAGTTTA	TAAGAGATGT	AGTGCGGGAA	· · · - <del>-</del>	1300
AGTACCGCCA	GGTACCTGGC	AGTGATCCCC	CAAGCTATGA	GTTCCTGTGG	1350

	GGACCCAGAG	CCCATGCTGA	AACAACCAAG	ATGAAAGTCC	TGGAAGTTTT	1400
	AGCTAAAGTC	AATGGCACAG	TCCCTAGTGC	CTTCCCTAAT	CTCTACCAGT	1450
	TGGCTCTTAG	AGATCAGGCA	GGAGGGGTGC	CAAGAAGGAG	AGTTCAAGGC	1500
	AAGGGTGTTC	ATTCCAAGGC	CCCATCCCAA	AAGTCCTCTA	ACATGTAGTT	1550
	GAGTCTGTTC	TGTTGTGTTT	GAAAAACAGT	CAGGCTCCTA	ATCAGTAGAG	1600
	AGTTCATAGC	CTACCAGAAC	CAACATGCAT	CCATTCTTGG	CCTGTTATAC	1650
	ATTAGTAGAA	TGGAGGCTAT	TTTTGTTACT	TTTCAAATGT	TTGTTTAACT	1700
	AAACAGTGCT	TTTTGCCATG	CTTCTTGTTA	ACTGCATAAA	GAGGTAACTG	1750
	TCACTTGTCA	GATTAGGACT	TGTTTTGTTA	TTTGCAACAA	ACTGGAAAAC	1800
	ATTATTTTGT	TTTTACTAAA	ACATTGTGTA	ACATTGCATT	GGAGAAGGGA	1850
	TTGTCATGGC	AATGTGATAT	CATACAGTGG	TGAAACAACA	GTGAAGTGGG	1900
	AAAGTTTATA	TTGTTAGTTT	TGAAAATTTT	ATGAGTGTGA	TTGCTGTATA	1950
	CTTTTTTCTT	TTTTGTATAA	TGCTAAGTGA	AATAAAGTTG	GATTTGATGA	2000
	CTTTACTCAA	ATTCATTAGA	AAGTAAATCA	TAAAACTCTA	TTACTTTATT	2050
,	ATTTTCTTCA	ATTATTAATT	AAGCATTGGT	TATCTGGAAG	TTTCTCCAG	2099

INFORMATION FOR SEQUENCE ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 9 amino acids
  - amino acids
- (D) TOPOLOGY: linear
  (ii) MOLECULE TYPE: protein
  (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Glu Ala Asp Pro Thr Gly His Ser Tyr